

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 22, 2003, 05:06:29 ; Search time 81 seconds
(without alignments)
4086.881 Million cell updates/sec

Title: US-09-978-273-2
Perfect score: 750
Sequence: 1 atgaaagaatagtgccaaa.....ctactgcgctgctaataa 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues
Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgm2_6/ptodata/2/ina/5A.COMB.seq.*
 - 2: /cgm2_6/ptodata/2/ina/5B.COMB.seq.*
 - 3: /cgm2_6/ptodata/2/ina/6A.COMB.seq.*
 - 4: /cgm2_6/ptodata/2/ina/6B.COMB.seq.*
 - 5: /cgm2_6/ptodata/2/ina/PCTUS.COMB.seq.*
 - 6: /cgm2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	740.8	98.8	847	1	US-08-378-761A-20
2	740.8	98.8	847	1	US-08-485-286-20
3	740.8	98.8	978	1	US-08-378-761A-10
4	740.8	98.8	978	1	US-08-485-286-10
5	740.8	98.8	985	1	US-08-378-761A-8
6	740.8	98.8	985	1	US-08-485-286-8
7	740.8	98.8	1161	1	US-08-378-761A-14
8	740.8	98.8	1161	1	US-08-485-286-14
9	740.8	98.8	1422	1	US-08-378-761A-16
10	740.8	98.8	1422	1	US-08-485-286-16
11	740.8	98.8	1683	1	US-08-378-761A-18
12	740.8	98.8	1683	1	US-08-485-286-18
13	740.8	98.8	1695	1	US-08-378-761A-22
14	740.8	98.8	1695	1	US-08-485-286-22
15	740.8	98.8	1722	1	US-08-378-761A-24
16	740.8	98.8	1722	1	US-08-485-286-24
17	737.8	98.4	1028	6	5248606-40
18	737.8	98.4	1029	1	US-08-378-761A-6
19	737.8	98.4	1029	1	US-08-485-286-6
20	720.2	96.0	987	1	US-08-378-761A-12
21	720.2	96.0	987	1	US-08-485-286-12
22	718.8	95.8	987	6	5248606-42
23	707.2	94.3	987	3	US-09-097-767A-5
24	655.8	87.4	1074	1	US-08-378-761A-4
25	655.8	87.4	1074	1	US-08-485-286-4
26	654.2	87.2	1059	3	US-09-097-767A-9
27	652.8	87.0	1076	1	US-08-378-761A-1

28	652.8	87.0	1076	1	US-08-485-286-1	Sequence 1, Appli
29	652.8	87.0	1105	1	US-08-378-761A-3	Sequence 3, Appli
30	652.8	87.0	1105	1	US-08-485-286-3	Sequence 3, Appli
31	652.8	87.0	1105	6	5248606-39	Patent No. 5248606
32	652.6	87.0	1053	3	US-09-097-767A-13	Sequence 13, Appli
33	651.2	86.8	1076	6	5248606-1	Patent No. 5248606
34	649.8	86.6	944	3	US-09-097-767A-16	Sequence 16, Appli
35	649.8	86.6	1244	3	US-09-097-767A-22	Sequence 22, Appli
36	636.8	84.9	1245	3	US-09-097-767A-25	Sequence 25, Appli
37	510.8	68.1	1934	1	US-07-941-651-1	Sequence 1, Appli
38	510.8	68.1	1934	1	US-08-279-996-1	Sequence 1, Appli
39	308	41.1	533	3	US-09-097-767A-36	Sequence 36, Appli
40	93	12.4	93	1	US-08-378-761A-39	Sequence 39, Appli
41	93	12.4	93	1	US-08-485-286-39	Sequence 39, Appli
42	77.6	10.3	846	1	US-07-901-707-12	Sequence 12, Appli
43	77.6	10.3	846	1	US-07-988-430-12	Sequence 12, Appli
44	77.6	10.3	846	1	US-08-425-336-12	Sequence 12, Appli
45	77.6	10.3	846	1	US-08-488-1138-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-378-761A-20
; Sequence 20, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46288
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 39272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51...845
US-08-378-761A-20

Query Match 98.8%; Score 740.8; DB 1; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.2e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAATCTCCCGTGAGGACGCGAAGTACCT 60

```
Db 51 ATGAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCT 110
Qy 61 TACAGCGCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGCAACGACCATATAA 120
Db 111 TACAGCGCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGCAACGACCATATAA 170
Qy 121 GGGATCTTCAGCCCGTGTGCGACCGGAGAAAGTCCCGAGCTATGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGTGTGCGACCGGAGAAAGTCCCGAGCTATGTTCTACACA 230
Qy 181 GAATCTGAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCGAT 240
Db 231 GAGCTCAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCGAT 290
Qy 241 GTGGCTTTCAGGACCCCGGGGCTGTGTGGAGTTCGGCAAGGACGCGGACACCCAC 300
Db 291 GTGGCTTTCAGGACCCCGGGGCTGTGTGGAGTTCGGCAAGGACGCGGACACCCAC 350
Qy 301 CTCTCGGCGACAAACCCAGTGTGCTGCGTTCGGCGGAGTTCGGCAAGGACGCGGACACCCAC 360
Db 351 CTCTCGGCGACAAACCCAGTGTGCTGCGTTCGGCGGAGTTCGGCAAGGACGCGGACACCCAC 410
Qy 361 AACAAAGGCTCGAGACCGTCAACATGGCGCGCGGATGCGCAAGGACGCGGACACCCAC 420
Db 411 AACAAAGGCTCGAGACCGTCAACATGGCGCGCGGATGCGCAAGGACGCGGACACCCAC 470
Qy 421 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGGACGCGGACGCGGACGCGGACGCGG 480
Db 471 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGGACGCGGACGCGGACGCGGACGCGG 530
Qy 481 CTGGTGTCTATGCTGCGAGGCGTCCGTTCAACCGGTTCGCGACGCGGACGCGGACGCGG 540
Db 531 CTGGTGTCTATGCTGCGAGGCGTCCGTTCAACCGGTTCGCGACGCGGACGCGGACGCGG 590
Qy 541 GGGTTCACAGCAGCAGCGGCTGACCTTGACCTTGACCTTGACCTTGACCTTGACCTTGACCT 600
Db 591 GGGTTCACAGCAGCAGCGGCTGACCTTGACCTTGACCTTGACCTTGACCTTGACCTTGACCT 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCC 660

RESULT 2
US-08-485-286-20
; Sequence 20, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 847 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..845
; US-08-485-286-20

Query Match 98.8%; Score 740.8; DB 1; Length 847;
Best Local Similarity 99.7%; Pred. No. 3.2e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCT 60
Db 51 ATGAAAGATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCT 110
Qy 61 TACAGCGCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGCAACGACCATATAA 120
Db 111 TACAGCGCTTTATCGGCTCGGTCCGGAAGACGTGATCAAACTGCAACGACCATATAA 170
Qy 121 GGGATCTTCAGCCCGTGTGCGACCGGAGAAAGTCCCGAGCTATGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGTGTGCGACCGGAGAAAGTCCCGAGCTATGTTCTACACA 230
Qy 181 GAATCTGAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCGAT 240
Db 231 GAGCTCAAACTAGACAGCTCCATCACCTGCCATGCGATGCGATGCGATGCGATGCGAT 290
Qy 241 GTGGCTTTCAGGACCCCGGGGCTGTGTGGAGTTCGGCAAGGACGCGGACACCCAC 300
Db 291 GTGGCTTTCAGGACCCCGGGGCTGTGTGGAGTTCGGCAAGGACGCGGACACCCAC 350
Qy 301 CTCTCGGCGACAAACCCAGTGTGCTGCGTTCGGCGGAGTTCGGCAAGGACGCGGACACCCAC 360
Db 351 CTCTCGGCGACAAACCCAGTGTGCTGCGTTCGGCGGAGTTCGGCAAGGACGCGGACACCCAC 410
Qy 361 AACAAAGGCTCGAGACCGTCAACATGGCGCGCGGATGCGCAAGGACGCGGACACCCAC 420
Db 411 AACAAAGGCTCGAGACCGTCAACATGGCGCGCGGATGCGCAAGGACGCGGACACCCAC 470
Qy 421 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGGACGCGGACGCGGACGCGGACGCGG 480
Db 471 CTGGCAAGAAAGAGGCGGTGACCTTCAAGGACGCGGACGCGGACGCGGACGCGGACGCGG 530
Qy 481 CTGGTGTCTATGCTGCGAGGCGTCCGTTCAACCGGTTCGCGACGCGGACGCGGACGCGG 540
Db 531 CTGGTGTCTATGCTGCGAGGCGTCCGTTCAACCGGTTCGCGACGCGGACGCGGACGCGG 590
Qy 541 GGGTTCACAGCAGCAGCGGCTGACCTTGACCTTGACCTTGACCTTGACCTTGACCTTGACCT 600
Db 591 GGGTTCACAGCAGCAGCGGCTGACCTTGACCTTGACCTTGACCTTGACCTTGACCTTGACCT 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCC 660
```

```
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
QY 661 GACATGCAAGCTTCGSCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 720
Db 711 GACATGCAAGCTTCGSCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 3
US-08-378-761A-10
; Sequence 10, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..815
US-08-378-761A-10

Query Match 98.8%; Score 740.8; DB 1; Length 978;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAATAGTGCAAGTTTCATGAAATCTCCCGTGGAGACGCGAACTACCT 60
Db 51 ATGAAAGAATAGTGCAAGTTTCATGAAATCTCCCGTGGAGACGCGAACTACCT 110
QY 61 TACAGCGCTTCATCGCTCGGTCGGAAGAGCTGATCAAACTGCGACCGCAATAA 120
Db 111 TACAGCGCTTCATCGCTCGGTCGGAAGAGCTGATCAAACTGCGACCGCAATAA 170
QY 121 GGGATCTTCAGCCCGTGTGTCGCCCGGAGAGAGAGTCCCGAGCTATGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGTGTGTCGCCCGGAGAGAGAGTCCCGAGCTATGTTCTACACA 230
```

```
QY 181 GAACTGAAAACTAGGACCAAGCTCCATCAAGCTCGCATAGCATGGAACACCTGTACTTC 240
Db 231 GAGCTCAAACTAGGACCAAGCTCCATCAAGCTCGCATAGCATGGAACACCTGTACTTC 290
QY 241 GTGGGCTTCAGAACCCCGGCGGGGTGCTGGAGGTTCCGCAAGGACGCGGACACCCAC 300
Db 291 GTGGGCTTCAGAACCCCGGCGGGGTGCTGGAGGTTCCGCAAGGACGCGGACACCCAC 350
QY 301 CTCCTCGGCGCAACCCAGAGTGGCTCGGCTTCGGGGGCGAGGTACAGAGCTCATCGGC 360
Db 351 CTCCTCGGCGCAACCCAGAGTGGCTCGGCTTCGGGGGCGAGGTACAGAGCTCATCGGC 410
QY 361 AACAGGGTCTCGAGACCGCTCAACATGGGCCCGCGCGAAATGACAGGGCGCTCAACGAC 420
Db 411 AACAGGGTCTCGAGACCGCTCAACATGGGCCCGCGCGAAATGACAGGGCGCTCAACGAC 470
QY 421 CTGGCGAAGAAAGAAAGCGGCTGACCCACAGGCGCGACACGAAAGCAAGCTGTGAAAG 480
Db 471 CTGGCGAAGAAAGAAAGCGGCTGACCCACAGGCGCGACACGAAAGCAAGCTGTGAAAG 530
QY 481 CTGGTGGTTCATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGG 540
Db 531 CTGGTGGTTCATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGG 590
QY 541 GGGTTCAAACAGCCAGCACCGGGGTGACCTTGACCGTGACGAGGGGAGCAGGTGCAGAG 600
Db 591 GGGTTCAAACAGCCAGCACCGGGGTGACCTTGACCGTGACGAGGGGAGCAGGTGCAGAG 650
QY 601 TGGGACAGGATCTCAAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCAAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
QY 661 GACATGCAAGCTTCGSCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 720
Db 711 GACATGCAAGCTTCGSCATCAAGGATAAGAAAGCAAGCAGGAGGATCGTTGCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
Db 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 4
US-08-485-286-10
; Sequence 10, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..815
US-08-378-761A-10
```

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BORUCKI, ANDREA T
/ REGISTRATION NUMBER: 33651
/ REFERENCE/DOCKET NUMBER: 38272B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 337-4846
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 978 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 51..815
/ US-08-485-286-10

Query Match      98.8%; Score 740.8; DB 1; Length 978;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATGAAAAGAAATAGTGCCAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCCCT 60
Db      |||||||
QY      51 ATGAAAAGAAATAGTGCCAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCCCT 110
Db      |||||||
QY      61 TACAGCGCTTCATCGCGTCCGGAAGAGCTGATCAAAACACTGCAACCGACCAATAAA 120
Db      |||||||
QY      111 TACAGCGCTTCATCGCGTCCGGAAGAGCTGATCAAAACACTGCAACCGACCAATAAA 170
Db      |||||||
QY      121 GGGATCTCCAGCCGCTGTCACCGGAGAGAGGTCGCGAGGTATGTTCTACACA 180
Db      |||||||
QY      171 GGGATCTCCAGCCGCTGTCACCGGAGAGAGGTCGCGAGGTATGTTCTACACA 230
Db      |||||||
QY      181 GAACCTGAAACTAGGACCGCTCCATCAGCTCGCCATACGATGACCAACCTGTACCTC 240
Db      |||||||
QY      231 GAGCTCAAACTAGGACCGCTCCATCAGCTCGCCATACGATGACCAACCTGTACCTC 290
Db      |||||||
QY      241 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCCGGAAGACGCGGACACCCAC 300
Db      |||||||
QY      291 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCCGGAAGACGCGGACACCCAC 350
Db      |||||||
QY      301 CTCCTCGGCGACAAACCCGAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
Db      |||||||
QY      351 CTCCTCGGCGACAAACCCGAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 410
Db      |||||||
QY      361 AACAGGGTCTGAGACCGGTCACTATGGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 420
Db      |||||||
QY      411 AACAGGGTCTGAGACCGGTCACTATGGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 470
Db      |||||||
QY      421 CTGGCGAAGAAAGAAAGCGGCTGACCCAGGCGGACACGAGAGCGAAGCTGTGTAAG 480
Db      |||||||
QY      471 CTGGCGAAGAAAGAAAGCGGCTGACCCAGGCGGACACGAGGCGAAGCTGTGTAAG 530
Db      |||||||
QY      481 CTGGTGGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGCG 540
Db      |||||||
QY      531 CTGGTGGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGCG 590
Db      |||||||
QY      541 GGGTTCAACAGCCAGCACCGGGGTGACCTTTGACCGTGACGCGGGGAAGCAGGTGCAAGAAG 600
Db      |||||||
QY      591 GGGTTCAACAGCCAGCACCGGGGTGACCTTTGACCGTGACGCGGGGAAGCAGGTGCAAGAAG 650
Db      |||||||
QY      601 TGGGACAGGATCTTCAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Db      |||||||
QY      651 TGGGACAGGATCTTCAAGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
Db      |||||||
QY      661 GACATCAGAGCTTCGCGATCAGGATAGAGCAGGACGCGGATCGTGGCTCGTT 720
Db      |||||||
QY      711 GACATCAGAGCTTCGCGATCAGGATAGAGCAGGACGCGGATCGTGGCTCGTT 770
Db      |||||||
QY      721 AAGATCAAACTACTGCGCGTGC 744
Db      |||||||
QY      771 AAGATCAAACTACTGCGCGTGC 794
Db      |||||||
```

```
RESULT 5
US-08-378-761A-8
/ Sequence 8, Application US/08378761A
/ Patent No. 5635384
/ GENERAL INFORMATION:
/ APPLICANT: WALSH, TERENCE A
/ APPLICANT: HEY, TIMOTHY D
/ APPLICANT: MORGAN, ALICE ER
/ TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
/ TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
/ TITLE OF INVENTION: USING
/ NUMBER OF SEQUENCES: 81
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ANDREA T. BORUCKI
/ STREET: 9330 ZIONSVILLE ROAD
/ CITY: INDIANAPOLIS
/ STATE: IN
/ COUNTRY: US
/ ZIP: 46268
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/378,761A
/ FILING DATE: 26-JAN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BORUCKI, ANDREA T
/ REGISTRATION NUMBER: 33651
/ REFERENCE/DOCKET NUMBER: 38272B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 337-4846
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 985 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 37..822
/ US-08-378-761A-8

Query Match      98.8%; Score 740.8; DB 1; Length 985;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATGAAAAGAAATAGTGCCAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCCCT 60
Db      |||||||
QY      37 ATGAAAAGAAATAGTGCCAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCCCT 96
Db      |||||||
QY      61 TACAGCGCTTCATCGCGTCCGGAAGAGCTGATCAAAACACTGCAACCGACCAATAAA 120
Db      |||||||
QY      97 TACAGCGCTTCATCGCGTCCGGAAGAGCTGATCAAAACACTGCAACCGACCAATAAA 156
Db      |||||||
QY      121 GGGATCTTCAGCCGCTGTCACCGGAGAGAGGTCGCGAGCTATGTTCTACACA 180
Db      |||||||
QY      157 GGGATCTTCAGCCGCTGTCACCGGAGAGAGGTCGCGAGCTATGTTCTACACA 216
Db      |||||||
QY      181 GAACCTGAAACTAGGACCGAGTCCATCAGCTCGCCATACGATGACCAACCTGTACCTC 240
Db      |||||||
QY      217 GAGCTCAAACTAGGACCGAGTCCATCAGCTCGCCATACGATGACCAACCTGTACCTC 276
Db      |||||||
QY      241 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCCGGAAGACGCGGACACCCAC 300
Db      |||||||
QY      277 GTGGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTCCGGAAGACGCGGACACCCAC 336
Db      |||||||
QY      301 CTCCTCGGCGACAAACCCGAGGTGGCTCGGCTTCGGGGGAGGTACAGGACCTCATCGGC 360
Db      |||||||
QY      337 CTCCTCGGCGACAAACCCGAGGTGGCTCGGCTTCGGGGGAGGTACAGGACCTCATCGGC 396
Db      |||||||
```

361 AACAGGCTCTGGAGACCGCTCACCATGGCGCGCGCGGAAATGACAGGCGCGTCAACGAC 420
Db
397 AACAGGCTCTGGAGACCGCTCACCATGGCGCGCGCGGAAATGACAGGCGCGTCAACGAC 456
Qy
421 CTGGCGAAGAGAGAGAGGCGGCTGACCCACAGCCGACACAGAGCAAGCAAGCTGGTGAAG 480
Db
457 CTGGCGAAGAGAGAGAGGCGGCTGACCCACAGCCGACACAGAGCAAGCAAGCTGGTGAAG 516
Qy
481 CTGGTGTCTATGCTGTGGAGGGGCTGCGGTTCAACACCGTGTCCCGACAGGTCGACGCG 540
Db
517 CTGGTGTCTATGCTGTGGAGGGGCTGCGGTTCAACACCGTGTCCCGACAGGTCGACGCG 576
Qy
541 GGTTTCAACAGCCAGCAGCGGCTGACCTTGACCGTGAAGGGAAGCAAGCTGCAAGAG 600
Db
577 GGTTTCAACAGCCAGCAGCGGCTGACCTTGACCGTGAAGGGAAGCAAGCTGCAAGAG 636
Qy
601 TGGGACAGGATCTCCAGGCGGCTTCCAGTGGGCTGACACCCAGCGCTGTATCCCC 660
Db
637 TGGGACAGGATCTCCAGGCGGCTTCCAGTGGGCTGACACCCAGCGCTGTATCCCC 696
Qy
661 GACATGAGAGCTTGGCATCAAGGATAAGAAAGAGAGGAGGATGTTGGCTCGTT 720
Db
697 GACATGAGAGCTTGGCATCAAGGATAAGAAAGAGAGGAGGATGTTGGCTCGTT 756
Qy
721 AAGATCAAACTACTGCGGCTGCC 744
Db
757 AAGATCAAACTACTGCGGCTGCC 780

RESULT 6

US-08-485-286-8
; Sequence 8, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 37..822
US-08-485-286-8

Query Match 98.8%; Score 740.8; DB 1; Length 985;
Best Local Similarity 99.7%; Pred. No. 3.3e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAAGAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 60
Db 37 ATGAAAGAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCT 96
Qy 61 TACAGCGCTTTCAGCGTCCGGAAGAGAGTGTATCAAACTGCAACGAGCAATAA 120
Db 97 TACAGCGCTTTCAGCGTCCGGAAGAGAGTGTATCAAACTGCAACGAGCAATAA 156
Qy 121 GGGATCTTCCAGCCCGTGTGCTGCCACCGGAGAGAGTCCCGAGGTATGTTCTACACA 180
Db 157 GGGATCTTCCAGCCCGTGTGCTGCCACCGGAGAGAGTCCCGAGGTATGTTCTACACA 216
Qy 181 GAATGAAACTAGGACCGCTCCATCAAGCTCCCATAGCATGCAACCTGTACCTC 240
Db 217 GAGCTCAAACTAGGACCGCTCCATCAAGCTCCCATAGCATGCAACCTGTACCTC 276
Qy 241 GTGGGCTTTCAGGACCCCGGCGGGTGTGGTGGAGTTGGCAAGGACGCGACACCCAC 300
Db 277 GTGGGCTTTCAGGACCCCGGCGGGTGTGGTGGAGTTGGCAAGGACGCGACACCCAC 336
Qy 301 CTCTCGGCGACAAACCCAGTGGCTCGGCTTCGGGCGGAGGTACACAGGACCTCATCGGC 360
Db 337 CTCTCGGCGACAAACCCAGTGGCTCGGCTTCGGGCGGAGGTACACAGGACCTCATCGGC 396
Qy 361 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGGAAATGACAGGCGCGTCAAGGAC 420
Db 397 AACAGGGTCTGGAGACCGTCAACATGGCGCGCGCGGAAATGACAGGCGCGTCAAGGAC 456
Qy 421 CTGGCGAAGAGAGAGGCGGCTGACCCACAGCGCGGACACAGAGCAAGCTGGTGAAG 480
Db 457 CTGGCGAAGAGAGAGGCGGCTGACCCACAGCGCGGACACAGAGCAAGCTGGTGAAG 516
Qy 481 CTGGTGTCTATGCTGTGGAGGGGCTGCGGTTCAACACCGTGTCCCGACAGGTCGACGCG 540
Db 517 CTGGTGTCTATGCTGTGGAGGGGCTGCGGTTCAACACCGTGTCCCGACAGGTCGACGCG 576
Qy 541 GGGTTCAACAGCCAGCAGCGGCTGACCTTGAACCGTGAACGAGGGAAGCGGTGCAAG 600
Db 577 GGGTTCAACAGCCAGCAGCGGCTGACCTTGAACCGTGAACGAGGGAAGCGGTGCAAG 636
Qy 601 TGGGACAGGATCTCCAGGCGGCTTTCGAGTGGGCTGACACCCAGCGCTGTATCCCC 660
Db 637 TGGGACAGGATCTCCAGGCGGCTTTCGAGTGGGCTGACACCCAGCGCTGTATCCCC 696
Qy 661 GACATGAGAGCTTGGCATCAAGGATAAGAAAGAGAGGAGGATGTTGGCTCGTT 720
Db 697 GACATGAGAGCTTGGCATCAAGGATAAGAAAGAGAGGAGGATGTTGGCTCGTT 756
Qy 721 AAGATCAAACTACTGCGGCTGCC 744
Db 757 AAGATCAAACTACTGCGGCTGCC 780

RESULT 7

US-08-378-761A-14
; Sequence 14, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

;; TITLE OF INVENTION: USING
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: ANDREA T. BORUCKI
;; STREET: 9330 ZIONSVILLE ROAD
;; CITY: INDIANAPOLIS
;; STATE: IN
;; COUNTRY: US
;; ZIP: 46268
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,761A
;; FILING DATE: 26-JAN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BORUCKI, ANDREA T
;; REGISTRATION NUMBER: 33651
;; REFERENCE/DOCKET NUMBER: 38272B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (317) 337-4846
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1161 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 51..998
;;
US-08-378-761A-14

Query Match 98.8%; Score 740.8; DB 1; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 60
DB 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 110
QY 61 TACAGCGCTTCATCGCGTGGTTCGGAAGAGTGTCAAAACACATGCACTGCACCATATAA 120
DB 111 TACAGCGCTTCATCGCGTGGTTCGGAAGAGTGTCAAAACACATGCACTGCACCATATAA 170
QY 121 GGGATCTTCAGCCCGTGTGCGCACCGGAGAGAGTCCCGAGCTATGTTCTACACA 180
DB 171 GGGATCTTCAGCCCGTGTGCGCACCGGAGAGAGTCCCGAGCTATGTTCTACACA 230
QY 181 GAACCTGAAATAGGACCGGTCCATCAGCTCGCCATACGATGCAACACCTGTACCTC 240
DB 231 GAGCTCAAACCTAGGACCGGTCCATCAGCTCGCCATACGATGCAACACCTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGGGTGTGTGGAGTTCGGCAAGACCGCGACACCCAC 300
DB 291 GTGGGCTTCAGGACCCCGGGGGTGTGTGGAGTTCGGCAAGACCGCGACACCCAC 350
QY 301 CTCCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 360
DB 351 CTCCTCGGACACACCCAGGTGGCTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 410
QY 361 AACAAAGGCTCGAGACCGGTACCATGGCGCGCGGCAATGACACGAGGCGGTCAACGAC 420
DB 411 AACAAAGGCTCGAGACCGGTACCATGGCGCGCGGCAATGACACGAGGCGGTCAACGAC 470
QY 421 CTGGCGAAGAAAGAGCGGCTGACCCACAGCGCCGACACGAGAGCAAGTGGTGAAG 480
DB 471 CTGGCGAAGAAAGAGCGGCTGACCCACAGCGCCGACACGAGAGCAAGTGGTGAAG 530
QY 481 CTGGTGGTCTATGTTGCGAGGGGTCGGGTTCAACACCGTGTCCCGCAGCGTGGACGG 540

DB 531 CTGGTGGTCTATGTTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGACGCG 590
QY 541 GGGTTCAACAGCCAGCAGCGGGTGAACCTTGACCGTGAAGCGGGAAGCAGGTGCAGAAG 600
DB 591 GGGTTCAACAGCCAGCAGCGGGTGAACCTTGACCGTGAAGCGGGAAGCAGGTGCAGAAG 650
QY 601 TGGGACAGGATCTCAAGCGCGGCTTCGAGTGGGTGACCCACCCACCGCTGTGATCCCC 660
DB 651 TGGGACAGGATCTCAAGCGCGGCTTCGAGTGGGTGACCCACCCACCGCTGTGATCCCC 710
QY 661 GACATGACAGCTTGGCATCAAGGATAAGACGAGCAGCGAGGATGTTCCGCTCGTT 720
DB 711 GACATGACAGCTTGGCATCAAGGATAAGACGAGCAGCGAGGATGTTCCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCCGCTGCC 744
DB 771 AAGAATCAAACTACTGCCGCTGCC 794

RESULT 8
US-08-485-286-14
; Sequence 14, Application US/08485286
; Patent No. 5646026
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..998
;
US-08-485-286-14

Query Match 98.8%; Score 740.8; DB 1; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3.4e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCAACTACCT 60

Db 711 GACATCAGAAGCTTGGCATCAAGGATAAGAAAGCAGCGAGGATCGTTGGCTCGTT 770
QY 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 10
US-08-485-286-16
; Sequence 16, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1422 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..1256
; US-08-485-286-16

Query Match 98.8%; Score 740.8; DB 1; Length 1422;
Best Local Similarity 99.7%; Pred. No. 3.5e-152;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCAGAGTTCTACTGAAATCTTCCCGTGAGACGCGAACTACCT 60
Db 51 ATGAAAGAAATAGTGCAGAGTTCTACTGAAATCTTCCCGTGAGACGCGAACTACCT 110
QY 61 TACAGCGCTTCAATCGCTCGGTCCGGAAGACGTGATCAAACTGCACCGACCTATAA 120
Db 111 TACAGCGCTTCAATCGCTCGGTCCGGAAGACGTGATCAAACTGCACCGACCTATAA 170
QY 121 GGGATCTTCCAGCCCGTGTGTCGCCACCGGAGAGAGGTCCCGAGCTATGTTCTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGTCGCCACCGGAGAGAGGTCCCGAGCTATGTTCTACACA 230

QY 181 GAACTGAAAACCTAGGACAGCTTCCATCGCTCGCCATCGCATGCAACAACTGTACCTC 240
Db 231 GAGCTCAAAAACCTAGGACAGCTTCCATCGCTCGCCATCGCATGCAACAACTGTACCTC 290
QY 241 GTGGGCTTTCAGGACCCCGGGCGGGGTGTGGTGGAGTTCCGGGAAGACGCGACACCCAC 300
Db 291 GTGGGCTTTCAGGACCCCGGGCGGGGTGTGGTGGAGTTCCGGGAAGACGCGACACCCAC 350
QY 301 CTCCTCGGCGACAAACCCAGGTGGCTCGCTTCGGCGGAGGTACCGAGCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGGTGGCTTCGGCGGAGGTACCGAGCTCATCGGC 410
QY 361 AACAAAGGCTTTCAGGACCCCGGTTCACCATGGCGCGCGGAAATGACACAGGCCCTCAACGAC 420
Db 411 AACAAAGGCTTTCAGGACCCCGGTTCACCATGGCGCGCGGAAATGACACAGGCCCTCAACGAC 470
QY 421 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACGAGGAGAGCTGTGAAG 480
Db 471 CTGGCGAAGAGAAAGAGCGGCTGACCCACAGGCGCGACACGAGGAGAGCTGTGAAG 530
QY 481 CTGGTGGTTCATGGTGTGGAGGGGTGGGTTCAACACCGTGTCCGCGACGGTGGACGCG 540
Db 531 CTGGTGGTTCATGGTGTGGAGGGGTGGGTTCAACACCGTGTCCGCGACGGTGGACGCG 590
QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAA 600
Db 591 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAA 650
QY 601 TGGGACAGATCTCAAGCGGCGCTTCGAGTGGGTGACCCACCGCTGTGATCCCG 660
Db 651 TGGGACAGATCTCAAGCGGCGCTTCGAGTGGGTGACCCACCGCTGTGATCCCG 710
QY 661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGGATCGTTCGCTCGTT 720
Db 711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGGATCGTTCGCTCGTT 770
QY 721 AAGAATCAAACTACTGCGCTGCC 744
Db 771 AAGAATCAAACTACTGCGCTGCC 794

RESULT 11
US-08-378-761A-18
; Sequence 18, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B

Db	111	TACAGGCGCTTCATCGCGTCGGTCCGGAAGACGTGATCAAAACACTGCACCGACCATAAA	170
Qy	121	GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGGTCCCGAGGCTATGTTCTACACA	180
Db	171	GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGGTCCCGAGGCTATGTTCTACACA	230
Qy	181	GAACTGAAACTAGGACCAAGCTCCATCAGGCTCGCCATACGATGACCAACCTGTACCTC	240
Db	231	GAGCTCAAACTAGGACCAAGCTCCATCAGGCTCGCCATACGATGACCAACCTGTACCTC	290
Qy	241	GTGGGCTTCAGGACCCCGGCGGGGTGTGTGGAGTTTCGGCAAGAACCGCGGACACCCAC	300
Db	291	GTGGGCTTCAGGACCCCGGCGGGGTGTGTGGAGTTTCGGCAAGAACCGCGGACACCCAC	350
Qy	301	CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACCCAGGACCTCATCGGC	360
Db	351	CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACCCAGGACCTCATCGGC	410
Qy	361	AACAAGGCTCTGAGACCGTCAACATCGGCGCGCGGAAATGACACAGGCGCGTCAACGAC	420
Db	411	AACAAGGCTCTGAGACCGTCAACATCGGCGCGCGGAAATGACACAGGCGCGTCAACGAC	470
Qy	421	CTGGCGAAGAGAAAGCGGCTGACCCACAGGCGGACACGAAAGCAAGCTGGTGAAG	480
Db	471	CTGGCGAAGAGAAAGCGGCTGACCCACAGGCGGACACGAAAGCAAGCTGGTGAAG	530
Qy	481	CTGGTGTCTATGTTGTCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGCG	540
Db	531	CTGGTGTCTATGTTGTCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGCG	590
Qy	541	GGGTTCAACAGCCAGCACCGGGTGACCTTGACCGTGACGCGGGGAAGCAAGTGCAGAAG	600
Db	591	GGGTTCAACAGCCAGCACCGGGTGACCTTGACCGTGACGCGGGGAAGCAAGTGCAGAAG	650
Qy	601	TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACCCGCCACCCGCTGTGATCCCC	660
Db	651	TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACCCGCCACCCGCTGTGATCCCC	710
Qy	661	GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGGATCGTTGGCGTCGTT	720
Db	711	GACATGCAGAGCTTGGCATCAAGGATAAGAACGAGCAGGAGGATCGTTGGCGTCGTT	770
Qy	721	AAGAATCAAACTACTGCCGTGCC	744
Db	771	AAGAATCAAACTACTGCCGTGCC	794

Search completed: October 22, 2003, 06:51:36
Job time : 83 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 05:05:17 ; Search time 2048 Seconds

(without alignments)
8900.565 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

Sequence: 1 atgaagaagaatagtcacaa.....ctactgcgcgtgcctaataa 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611.6	81.5	3101	11 AY109436	AY109436 Zea mays
2	510.8	68.1	1155	11 AY104490	AY104490 Zea mays
3	490	65.3	748	14 CD433123	CD433123 EL01N0304
4	467	62.3	820	29 BZ720403	BZ720403 PUDAV35TD

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	460	61.3	798	14	CD448738	CD448738 EK07D2305
6	438.8	58.5	681	14	CD448132	CD448132 EK07D2303
7	437.4	58.3	752	29	BZ614599	BZ614599 i945d12.9
8	419.2	55.9	600	14	CD439415	CD439415 EL01N0524
9	370.8	49.4	562	10	BF481680	BF481680 FMI_21_A1
C 10	369.6	49.3	846	29	CC332989	CC332989 OGTAH31TV
C 11	348	46.4	672	14	CD448302	CD448302 EK07D2305
C 12	340	45.3	695	14	CD448545	CD448545 EK07D2303
C 13	336.6	44.9	366	14	TI18690	TI18690 5C04F01-T7
C 14	306	40.8	436	9	AI667697	AI667697 605026A04
C 15	306	40.8	573	9	AI664942	AI664942 605004F08
C 16	306	40.8	610	9	AI665398	AI665398 605010G04
C 17	304.4	40.6	522	9	AI833854	AI833854 605096D02
C 18	295	39.3	561	9	AI668230	AI668230 605018E05
C 19	284	37.9	600	10	BF481516	BF481516 FMI_21_A1
C 20	271.2	36.2	527	29	BZ799034	BZ799034 PUFCK38TD
C 21	270.2	36.0	458	14	CA04843	CA04843 EL01N0524
C 22	264.6	35.3	423	9	AW157976	AW157976 za31d10.X
C 23	258.4	34.5	478	28	BH638577	BH638577 1008023D0
C 24	254.8	34.0	515	28	BH414969	BH414969 1007040F0
C 25	244.8	32.6	403	14	T25265	T25265 5cl1d07 mem
C 26	237.6	31.7	576	10	BG559906	BG559906 RH1Z2_75
C 27	236.8	30.2	376	14	TI18677	TI18677 5C04B01-T7
C 28	234.6	29.9	504	10	BG559917	BG559917 RH1Z2_75
C 29	217.2	29.0	539	9	AW498398	AW498398 660047D10
C 30	215.8	28.8	419	28	BH638701	BH638701 1008024B0
C 31	215.6	28.7	516	12	BI993018	BI993018 1020071D1
C 32	215.6	28.7	682	29	BZ614598	BZ614598 i945d12.B
C 33	214.2	28.6	456	14	CA398486	CA398486 EL01N0304
C 34	212	28.3	436	28	BH629418	BH629418 1007072C0
C 35	208.4	27.8	361	9	AI670370	AI670370 605022F01
C 36	190	25.3	460	28	BH629453	BH629453 1007072F0
C 37	180.8	24.1	507	10	BG517901	BG517901 947064D04
C 38	176.8	23.6	450	14	TI18631	TI18631 5C07a12-C7
C 39	176.6	23.5	485	12	BG836402	BG836402 Zm06_01h0
C 40	173	23.1	655	14	CA604530	CA604530 wr1.pk004
C 41	160.8	21.4	391	14	T23398	T23398 5C09d11 mem
C 42	142.2	19.0	318	13	BQ655923	BQ655923 PR00037_S
C 43	129	17.2	271	28	BH628746	BH628746 1007084G0
C 44	128.8	17.2	227	28	BH629588	BH629588 1007073E0
C 45	128.4	17.1	219	28	BH407893	BH407893 1007051H0

ALIGNMENTS

RESULT 1	AY109436	AY109436	3101 bp	mRNA	linear	HTC 17-OCT-2002
LOCUS	Zea mays CL1124_1 mRNA sequence.					
DEFINITION	Zea mays CL1124_1 mRNA sequence.					
ACCESSION	AY109436					
VERSION	AY109436.1					GI:21213157
KEYWORDS	HTC.					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD					
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 3101)					
AUTHORS	Coe, E.H.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the					

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source
Location/Qualifiers
1..3101
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:630000"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="This sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 733 a 565 c 645 g 632 t 526 others
ORIGIN
Query Match 81.5%; Score 611.6; DB 11; Length 3101;
Best Local Similarity 87.2%; Pred. No. 7.6e-129; Indels 78; Gaps 1;
Matches 714; Conservative 0; Mismatches 27;
QY 4 AAAAGATAGTCCCAAGTTCACTGAAATCTTCCCGTGGAGGACGGAATACCTTAC 63
Db 1696 AACAAAAGATAGTCACTGAAATCTTCCCGTGGAGGACGGAATACCTTAC 1755
QY 64 AGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAACACTGACCGACCATTAAGG 123
Db 1756 AGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAACACTGACCGACCATTAAGG 1815
QY 124 ATCTTCCAGCCGCTGCTCCACCGAGAGAGGTCCCGAGCTATGTTCTACACAGAA 183
Db 1816 ATCTTCCAGCCGCTGCTCCACCGAGAGAGGTACCGAGCTGTTGTTTACAGGAG 1875
QY 184 CTGAAAATAGAACACGCTCCATCAGCTCGCATACGATGACGACCACTGTACCTGTG 243
Db 1876 CTGAAAATAGAACACGCTCCATCAGCTCGCATACGATGACGACCACTGTACCTGTG 1935
QY 244 GCCTTCAGAACCCCGGGGGGTGTGGTGGAGTTCCGGAAGAGACGGGACACCCACCTC 303
Db 1936 GCCTTCAGAACCCCGGGGGGTGTGGTGGAGTTCCGGAAGAGACGGGACACCCACCTC 1995
QY 304 CTCGGCGCAACCCAGGTGGCTCGGCTTCGCGGACGATACGAGACCTCATCGCAAC 363
Db 1996 CTCGGCGCAACCCAGGTGGCTCGGCTTCGCGGACGATACGAGACCTCATCGCAAC 2055
QY 364 AAGGCTCTGGAGACCGTCAACATGGGCGCGCGGAATGACACGGGCGGTCAACGACCTG 423
Db 2056 AAGGCTCTGGAGACCGTCAACATGGGCGCGCGGAGATGACACGGGCGGTCAACGACCTG 2115
QY 424 CGGAGAGAGAA----- 437
Db 2116 CGGAGAGAGAGATGGCGGACACTGGAGGAGGAGGTGACAGTGCAGATGCAGATG 2175
QY 438 -----GGCGGTGACCCACAGCGCGACAGAG 465
Db 2176 CGGAGGCGGCTGATCTGGCGCGGCGGACGCGGTGANNCCACAGCGCGACAGAG 2235
QY 466 AGCAAGCTGGTGAAGTGGTGTATGTGTGTCGAGGGGCTCGGTTCAACACCGTGTCC 525
Db 2236 AGCAAGCTGGTGAAGTGGTGTATGTGTGTCGAGGGGCTCGGTTCAACACCGTGTCC 2295
QY 526 CGCAGGTGGACCGGGTTCAACAGCAGCAGCGGGTGACCTTACCGTGAACGAGGG 585
Db 2296 CGCAGGTGGACCGGGTTCAACAGCAGCAGCGGGTGACCTTACCGTGAACGAGGG 2355
QY 586 AAGCAGGTGACAGTGGGACAGGATCTCCAGGGCGGCTTCGAGTGGGCTGACACCCC 645
Db 2356 AAGCAGGTGACAGTGGGACAGGATCTCCAGGGCGGCTTCGAGTGGGCGGACACCCC 2415
QY 646 ACCGCTGTATCCCCGACATGCAGAGCTTGGCATCAAGGATAGAAGACGAGCGAGG 705

Db 2416 ACCGCTGTATCCCCGACATGCAGAGCTTGGCATCAAGATAAGACGAGCGAGG 2475
QY 706 ATCGTTGGCTCGTTAAGATCAAACTACTGCCCGCTGCC 744
Db 2476 ATCGTTGGCTCGTTAAGATCAAACTACTGCCCGCTGCC 2514
RESULT 2
AY104490 1155 bp mRNA linear HTC 16-OCT-2002
LOCUS Zea mays PC0148580 mRNA sequence.
DEFINITION AY104490
ACCESSION AY104490
VERSION AY104490.1 GI:21207568
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1155)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
AUTHORS 2 (bases 1 to 1155)
Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSI, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES
Location/Qualifiers
1..1155
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:638767"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 327 a 308 c 308 g 212 t
ORIGIN
Query Match 68.1%; Score 510.8; DB 11; Length 1155;
Best Local Similarity 80.7%; Pred. No. 5.2e-106;
Matches 633; Conservative 0; Mismatches 97; Indels 54; Gaps 1;
QY 1 ATGAAAAGATAGTGCACAAAGTTCACGAAATCTTCCCGTGGAGGACGGAATACCT 60
Db 109 AAGAAAATATAGTGCACAAAGTTCACGAAATCTTCCCGTGGAGGACGCGCTACCT 168
QY 61 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAACACTCCACGACCATATA 120
Db 169 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAACACTCCACGACCATATA 228
QY 121 GGGATCTTCCAGCCGCTGTCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACA 180
Db 229 GGCATCGTCCAGCCGCTGTCCCGTGGAGAGAGATGTCCCGAGCTCTGTTCTACAC 288
QY 181 GAATGAAAATAGGACAGCTCCATCAGCTCCGCTCCCATACGATGGACACCTGTACTC 240

```
Db      289 GAGCTCAAAACGAAGACACGAGTCCATCACGCTCGCCATACGATATGGAACAACCTCTACCTG 348
Qy      241 GTGGGCTTCAGAGACCCCGGGCGGGTGTGTGGAGTTTCGCAAGAGCGGCGACACCCAC 300
Db      349 GTCGGCTTCAGAGACCCCGGGCGGGTGTGTGGAGTTTCGCAAGAGCGGCGACACCCAC 408
Qy      301 CTCCTCGCGCAGAACCCCGAGTGGCTCGGCTTCGGCGCGAGTACCAGGACTCATCGGC 360
Db      409 CTCCTCGAGGACAGCCCAAGTGGCTCGGCTTCGGCGCGGTACCAGGACTCATCGGC 468
Qy      361 AACAAAGGCTTCGAGACCGTCAACATGGGCGCGCGGAAATGACACAGGCGCGTCAACGAC 420
Db      469 AGTAAGGCGCTGGAGACCGTCAACATGGGCGGTGCGGAAATGACACAGGCGGTCAACTAC 528
Qy      421 CTGCGGAGAGAGAGAAG----- 438
Db      529 CTGGCGAAGAGACACGACGACATAGCAGAGCGCGGAGGAGGAGGAGAGTGTGTG 588
Qy      439 -----GCGGCTGACCCAGCCAGCGCCGACAGAGCAAGAGCAAGCTGTGTAAGTGTG 486
Db      589 CTGCTGCGAGGCGAGCGGCTGACCCAAAGCGGAGGAGAGCAACCTTGGCGAAGCTAGTG 648
Qy      487 GTCATGTGTGGAGGGCTGGGTTCAACACCGTGTCCGCGACCGTGGACCGCGGGTTC 546
Db      649 ATCATGTGTATGAGGGGCTGGCGTTCTTCAACCGTGTCCCGCAAGGTAGACGAGGGGTTT 708
Qy      547 AACAGCCAGCAGCGGGGTGACCTTGACGTGAGCGAGGAGGAGAGCAGTGCAGAAAGTGGAC 606
Db      709 AAGAGCGCGAAGCGGTGACATATCGGCGTGGAGGGGAGAGAGTGCAGAAATGGGAC 768
Qy      607 AGGATCTCCAAAGCGCGCTTCAGTGGGCTGACCAACCCCGCTGTGATCCCGACATG 666
Db      769 AGGATCTCGAAGCGCTTTCAGTGGCGCGTGCAGCCGCTGAGATCCCGACATG 828
Qy      667 CAGAGCTTGGCATCAAGGATAGAAAGAGAGAGAGAGTGGTGGCTGTGCTGTAAAGAT 726
Db      829 AAGGATCTTGGCATCAAGATAAAGAACGAGCAGCGAGATCGTGGCTGTGTTAAGGAC 888
Qy      727 CAAA 730
Db      889 CAAA 892

RESULT 3
CD433123 748 bp mRNA linear EST 03-JUN-2003
LOCUS EL01N0304G01.b EndospERM_3 Zea mays cDNA, mRNA sequence.
DEFINITION CD433123
ACCESSION CD433123
VERSION CD433123.1 GI:31348766
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 748)
AUTHORS Lai, J., Dey, N., Kim, C.S., Beecraft, P., Larkins, B., Linton, E. and
Messing, J.
Sequencing of the maize endospERM ESTs
JOURNAL Unpublished
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
source 1..748
/mol_type="mRNA"
/cultivar="W22"
```

```
/db xref="taxon:4577"
/tissue_type="EndospERM of 7-23DAP"
/clone_lib="EndospERM_3"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 171 a 213 c 244 g 120 t
ORIGIN
Query Match 65.3%; Score 490; DB 14; Length 748;
Best Local Similarity 87.8%; Pred. No. 2.5e-101;
Matches 578; Conservative 0; Mismatches 5; Indels 75; Gaps 1;
Qy 162 GGAGCTATGTTCTACACAGAACTGAAACTAGGACACAGCTCCATCACTCGCTCGCATACG 221
Db 1 GGAGCTATGTTCTACACAGAGCTCAAACTAGGACACAGCTCCATCACTCGCTCGCATACG 60
Qy 222 CATGGAACAACCTGTACCTGTGGGCTTCAGAACCCCGGGCGGGTGTGTGGAGTTCGG 281
Db 61 CCTCAACAACCTGTACCTGTGGGCTTCAGAACCCCGGGCGGGTGTGTGGAGTTCGG 120
Qy 282 CAAGGACGGGACACCCACCTCTCGCGCAACCCAGGTTGGCTCGGCTTCGCGCGGACG 341
Db 121 CAAGGACGGGACACCCACCTCTCGCGCAACCCAGGTTGGCTCGGCTTCGCGCGGACG 180
Qy 342 GTACGAGACCTCATCGGCAACAAGGTTCTGGAGACCGTCAACCATGGGCCCGCGCAAT 401
Db 181 GTACGAGACCTCATCGGCAACAAGGTTCTGGAGACCGTCAACCATGGGCCCGCGCAAT 240
Qy 402 GACGAGGCGCTCAACGACCTGGGCAAGAGAAAG----- 438
Db 241 GACGAGGCGCTCAACGACCTGGGCAAGAGAAAGATGTCGTTTCTGGAGGAGGAGGA 300
Qy 439 -----GCGGCTGA 446
Db 301 GGTGAGATGAGATGAGATGCGAGTGCAGGAGCGCGTGTATCTGCGGCGGCGGAGCGGCTGA 360
Qy 447 CCCACAGCGCGACAGCAAGAGCAAGCTGTGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 506
Db 361 CCCACAGCGCGACAGCAAGAGCAAGCTGTGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 507 GCGGTTCAACACCGTGTCCGCGACGCGTGTGATCCCGGACATGCGAGCATGCGAGCGGGTAC 566
Db 421 GCGGTTCAACACCGTGTCCGCGACGCGTGTGATCCCGGACATGCGAGCATGCGAGCGGGTAC 480
Qy 567 CTTGACCGTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 626
Db 481 CTTGACCGTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
Qy 627 CGAGTGGGCTGACCAACCCCGCTGTGATCCCGGACATGCGAGCATGCGAGCATGCGAGG 686
Db 541 CGAGTGGGCTGACCAACCCCGCTGTGATCCCGGACATGCGAGCATGCGAGCATGCGAGG 600
Qy 687 TAAGAACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 744
Db 601 TAAGAACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 658

RESULT 4
EZ720403 820 bp DNA linear GSS 24-FEB-2003
LOCUS PUDAV35TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMB7a145E22,
DEFINITION genomic survey sequence.
ACCESSION BZ720403
VERSION BZ720403.1 GI:28510832
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 820)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick
A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
```



```

TITLE      Maize Genomics Consortium
JOURNAL    Unpublished
COMMENT    Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: IF
          Class: sheared ends.
FEATURES   Location/Qualifiers
            1..820
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBT4145822"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
            CoT selected genomic DNA library"
BASE COUNT 197 a 224 c 256 g 143 t
ORIGIN
Query Match      62.3%; Score 467; DB 29; Length 820;
Best Local Similarity 88.0%; Pred. No. 4.4e-96;
Matches 552; Conservative 0; Mismatches 0; Indels 75; Gaps 1;
QY 193 AGGACAGCTCCATCAGCTCCGCATACGCATGGACACCTGTACTCTGTGGGCTTCAGG 252
   |||||
Db 1 AGGACAGCTCCATCAGCTCCGCATACGCATGGACACCTGTACTCTGTGGGCTTCAGG 60
QY 253 ACCCGGGGGGGTGTGGGAGTTTCGGCAAGGACGGGACACCCACCTCTCTCGGCGAC 312
   |||||
Db 61 ACCCGGGGGGGTGTGGGAGTTTCGGCAAGGACGGGACACCCACCTCTCTCGGCGAC 120
QY 313 AACCCCAAGTGGCTCGGCTTCGGCGGACGGTACCGACCTTCATCGGCAACAGGTTCTG 372
   |||||
Db 121 AACCCCAAGTGGCTCGGCTTCGGCGGACGGTACCGACCTTCATCGGCAACAGGTTCTG 180
QY 373 GAGACCGTCCATATGGCGCGCGGAAATGACAGGGCCGTCAACGACTTGGCGAAGAG 432
   |||||
Db 181 GAGACCGTCCATATGGCGCGCGGAAATGACAGGGCCGTCAACGACTTGGCGAAGAG 240
QY 433 AAGAG----- 438
   |||||
Db 241 AAGAGATGGACACTGGAGGAGGAGGTGCAGATGCAGATGCCGAGGCC 300
QY 439 -----GCGGCTGACCCACAGGCCGACACGAGGCAAGCAAGCTGGTG 477
   |||||
Db 301 GCTGATCTGGCGGCGCGCAGCGGCTGACCCACAGGCGGACACGAAAGAGCAAGCTGGTG 360
QY 478 AAGCTGGTGTATGTTGCGAGGGGCTCGGTTCAACACCGTGTCCGCGACGGTGAC 537
   |||||
Db 361 AAGCTGGTGTATGTTGCGAGGGGCTCGGTTCAACACCGTGTCCGCGACGGTGAC 420
QY 538 GCGGGGTTCAACAGCCAGCACGCGGTGACCTTGACCGTGCACGAGGGGAAGCAGGTGCAG 597
   |||||
Db 421 GCGGGGTTCAACAGCCAGCACGCGGTGACCTTGACCGTGCACGAGGGGAAGCAGGTGCAG 480
QY 598 AAGTGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATC 657
   |||||
Db 481 AAGTGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATC 540
QY 658 CCGGACATGCAGAACTTGGCATCAAGGATAAGAAAGGAGCAGGATCGTTGGCTC 717
   |||||
Db 541 CCGGACATGCAGAACTTGGCATCAAGGATAAGAAAGGAGCAGGATCGTTGGCTC 600
QY 718 GTTAAAGATCAAACTACTGCGCTGCC 744
   |||||
Db 601 GTTAAAGATCAAACTACTGCGCTGCC 627
QY
RESULT 5

```

```

CD448738
LOCUS      EX07D2305H08.b EndospERM_6 Zea mays cDNA, mRNA linear EST 03-JUN-2003
DEFINITION CD448738
ACCESSION  CD448738
VERSION    CD448738.1 GI:31364383
KEYWORDS   EST.
SOURCE     Zea mays
           Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 798)
AUTHORS   Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
           Messing,J.
TITLE      Sequencing of the maize endospERM ESTs
JOURNAL    Unpublished
COMMENT    Contact: Lai, Jinsheng
           Dr. Joachim Messing's lab
           Waksman Institute, Rutgers University
           190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
           Tel: 732-445-3801
           Fax: 732-445-5735
           Email: jlai@waksman.rutgers.edu
           Seq primer: T3.
FEATURES   Location/Qualifiers
            1..798
            /organism="Zea mays"
            /mol_type="mRNA"
            /cultivar="W22"
            /db_xref="taxon:4577"
            /tissue_type="EndospERM of 7-23 DAP"
            /clone_lib="EndospERM 6"
            /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI"
BASE COUNT 196 a 219 c 255 g 127 t
ORIGIN
Query Match      61.3%; Score 460; DB 14; Length 798;
Best Local Similarity 87.9%; Pred. No. 1.7e-94;
Matches 545; Conservative 0; Mismatches 0; Indels 75; Gaps 1;
QY 200 GCTCATCAGCTCCGCATACGCATGGACACCTGTACTCTGTGGGCTTCAGGACCCCGG 259
   |||||
Db 8 GCTCATCAGCTCCGCATACGCATGGACACCTGTACTCTGTGGGCTTCAGGACCCCGG 67
QY 260 GCGGGGTGTGTGGAGTTTCGGCAAGGACGGGACACCTCTCTCGGCAACACCCCA 319
   |||||
Db 68 GCGGGGTGTGTGGAGTTTCGGCAAGGACGGGACACCTCTCTCGGCAACACCCCA 127
QY 320 GGTGCTCGGCTTCGGCGGACAGTACCAGGACCTCATCGGCAACAGGCTTCGGAGACCG 379
   |||||
Db 128 GGTGCTCGGCTTCGGCGGACAGTACCAGGACCTCATCGGCAACAGGCTTCGGAGACCG 187
QY 380 TCACCATGGCGCGCGGAATGACGAGGCGGTCAACACCGTTCGCCGACGGTGCAGAGAGAGAG- 438
   |||||
Db 188 TCACCATGGCGCGCGGAATGACGAGGCGGTCAACACCGTTCGCCGACGGTGCAGAGAGAGAG- 247
QY 439 ----- 438
   |||||
Db 248 TGGCACACTGAGAGGAGGAGGTGCAGATGCAGATGCCGAGCGCGCTGATC 307
QY 439 -----CGGGCTGACCCACAGGCGCGACACGAGAGCAAGCTGTGTGAAGCTGG 484
   |||||
Db 308 TGGCGGCGGCGGACGCGCTGACCCACAGGCGGACACGAGAGCAAGCTGTGTGAAGCTGG 367
QY 485 TGGTCATGTTGCGAGGGGCTGCGGTTCAACACCGTTCGCCGACGGTGCAGAGAGTGGG 544
   |||||
Db 368 TGGTCATGTTGCGAGGGGCTGCGGTTCAACACCGTTCGCCGACGGTGCAGAGAGTGGG 427
QY 545 TCACAGCCAGCACGCGGTTGACCTTTGACCGTACCGAGGGGAAGCAGGTTGCAGAAAGTGGG 604
   |||||
Db 428 TCACAGCCAGCACGCGGTTGACCTTTGACCGTACCGAGGGGAAGCAGGTTGCAGAGAGTGGG 487
QY 605 ACAGGATCTCCAAGGCGGCGCTTCGAGTGGGCTTGAACACCCACCGCTGTGATCCCCGACA 664
   |||||

```

```

Db      488 ACAGGATCTCCAAAGCGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCGACA 547
Qy      665 TCAGAGAGCTTGGCATCAAGGTAAGAACAGAGCAGCAGGAGTCTGTGGCGCTCGTTAAGA 724
Db      548 TCAGAGAGCTTGGCATCAAGGTAAGAACAGAGCAGCAGGAGTCTGTGGCGCTCGTTAAGA 607
Qy      725 ATCAAACTACTGCGCGTGC 744
Db      608 ATCAAACTACTGCGCGTGC 627

RESULT 6
CD448132
LOCUS      CD448132      681 bp      mRNA      linear      EST 03-JUN-2003
DEFINITION EK07D22303A09.g Endosperm_6 Zea mays cDNA, mRNA sequence.
ACCESSION  CD448132
VERSION     CD448132.1 GI:31363775
KEYWORDS
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 681)
AUTHORS     Lai,J., Dey,N., Kim,C.S., Becraft,P., Larkins,B., Linton,E. and
            Messing,J.
TITLE       Sequencing of the maize endosperm ESTs
JOURNAL
COMMENT     Contact: Lai, Jinsheng
            Dr. Joachim Messing's lab
            Waksman Institute, Rutgers University
            190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
            Tel: 732-445-3801
            Fax: 732-445-5735
            Email: jlai@waksman.rutgers.edu
            Seq primer: T7.

FEATURES
            Location/Qualifiers
            1..681
               /organism="Zea mays"
               /mol_type="mRNA"
               /cultivar="W22"
               /db_xref="taxon:4577"
               /tissue type="Endosperm of 7-23 DAP"
               /clone lib="Endosperm 6"
               /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT  174 a 189 c 213 g 103 t
ORIGIN
Query Match      58.5%; Score 438.8; DB 14; Length 681;
Best Local Similarity 94.0%; Pred. No. 1.1e-89;
Matches 455; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy      4 AAAAGAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGAGCGCAACTACCTTAC 63
Db      101 AAAAGAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGAGCGCAACTACCTTAC 160
Qy      64 AGCGCTTCATCGCTCGCTCCGGAAGACGTTGATCAACACTGACACCGACCAATAAGGG 123
Db      161 AGCGCTTCATCGCTCGCTCCGGAAGACGTTGATCAACACTGACACCGACCAATAAGGG 220
Qy      124 ATCTTCACGCCCGTGTGCCACCGGAGAAAGGTCCCGGAGCTATGTTCTACAGAAA 183
Db      221 ATCTTCACGCCCGTGTGCCACCGGAGAAAGGTCCCGGAGCTATGTTCTACAGAG 280
Qy      184 CTGAAGACTAGGACACAGCTCCATCACTCGCCATACGATGACAACTGTACCTCGTG 243
Db      281 CTGAAGACTAGGACACAGCTCCATCACTCGCCATACGATGACAACTGTACCTCGTG 340
Qy      244 GCCTTCAGACCCCGCGGGGTGTGGAGTTTCGGCAAGCAGCGGCACACCCACCTC 303
Db      341 GCCTTCAGACCCCGCGGGGTGTGGAGTTTCGGCAAGCAGCGGCACACCCACCTC 400

```

```

Qy      304 CTCGGCGCAAAACCCAGGTGGCTTCGGCGCGCAGGTACCGAGCACTCATCGGCAAC 363
Db      401 CTCGGCGCAAAACCCAGGTGGCTTCGGCGCGCAGGTACCGAGCACTCATCGGCAAC 460
Qy      364 AAGGTCCTGGAGACCGTCAACCATGGCGCGCCGAAATGACCGAGCGCGTCAACGACCTG 423
Db      461 AAGGTCCTGGAGACCGTCAACCATGGCGCGCCGAAATGACCGAGCGCGTCAACGACCTG 520
Qy      424 CGGAGAGAGAGAGGCGGCTGACCCACAGCCCGACACGAAGAGCAAGCTGCTGAAGCTG 483
Db      521 CGGAGAGAGAGAGATGGCGCACTGGAGGAGGAGGAGTGCANATGCANATGCAGATG 580
Qy      484 GTGG 487
Db      581 CCGG 584

RESULT 7
BZ614599
LOCUS      BZ614599      752 bp      DNA      linear      GSS 16-JAN-2003
DEFINITION ig45dl12.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ACCESSION  BZ614599
VERSION     BZ614599.1 GI:27765154
KEYWORDS
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 752)
AUTHORS     Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,
            Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
            Zutavern,T., McCombie,W.R. and Martienssen,R.A.
            Genomic shotgun sequences from Zea mays (methyl-filtered)
            Unpublished
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mcombie@cshl.org
            Plate: ig45 row: d column: 12
            Seq primer: -21M13UnivRev
            Class: shotgun
            High quality sequence stop: 752.
            Location/Qualifiers
            1..752
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="B73"
               /db_xref="taxon:4577"
               /clone="ig45dl12"
               /lab host="DH5a"
               /clone lib="WGS-ZmaysF (DH5a methyl filtered)"
               /note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
            The vector was digested with XbaI and one nucleotide was
            added by fill in in the recessive 3' end. The genomic DNA
            was nebulized, end repaired, adaptor ligated and size
            fractionated using sephadex. The resulting fragments were
            between 0.8 and 3 kb and were cloned into the vector (.x/y
            reads in M13mpl9, .b/g reads in pUC19). The same ligation
            was transformed into DH5a."
BASE COUNT  180 a 215 c 237 g 120 t
ORIGIN
Query Match      58.3%; Score 437.4; DB 29; Length 752;
Best Local Similarity 79.3%; Pred. No. 2.4e-89;
Matches 556; Conservative 0; Mismatches 91; Indels 54; Gaps 1;

Qy      84 CCGGAAAGACGTTGATCAAAACACTGACCGACCAATAAAGGATCTTCCAGCCCGCTCGCC 143

```

```
Db 24 CTTCCGAGGAGTGATCAAAATACCTGACCAACCATACAGGATCGTCCAGCCGCTGCTGCC 83
QY 144 ACGGAGAGAGAGTCCCGAGCTATGTTTACACAGAACTCAAAACTAGGACCAAGCTC 203
Db 84 GTTGGAGAAGATGTCCTCCGAGCTCTGGTTCACACGAGCTCAAAACGAAGACAGGTC 143
QY 204 CATCAGCTCGCCATACGATGATGACAACTGTACCTCGTGGGCTTCAGACCCCGGGCGG 263
Db 144 CATCAGCTCGCCATACGATGATGACAACTGTACCTCGTGGGCTTCAGACCCCGGGCGG 203
QY 264 GTTGTGGTGGAGTTTCGGCAAGACCGCGACACCCACCTCTCTCGACGACAAACGCAAGTG 323
Db 204 GTTGTGGTGGAGTTTCGGCAAGACCGCGACACCCACCTCTCTCGACGACAAACGCAAGTG 263
QY 324 GTTGTGGTGGAGTTTCGGCAAGACCGCGACACCCACCTCTCTCGACGACAAACGCAAGTG 323
Db 264 GTTGTGGTGGAGTTTCGGCAAGACCGCGACACCCACCTCTCTCGACGACAAACGCAAGTG 263
QY 384 CATGGCCCGCGCGAAATGACAGGCGCGTCAACGACCTGGCGGAGAAAGAAAG----- 438
Db 324 CATGGCCCGCGCGAAATGACAGGCGCGTCAACGACCTGGCGGAGAAAGAAAG----- 438
QY 439 -----GCGGCTGACCC 449
Db 384 ACTAGCAGAGGCGCGAGGAGGAGGAGGAGTCTGTCTGTCAGGCGAGCGCTGACCC 443
QY 450 ACAGGCGCGACACAGAGCAAGCTGTGAAGCTGTGTGTCATGTTGTGCGAGGGGCTGG 509
Db 444 CAAGCCGAGGAGAGAGCAACTGCGGAAGCTGTGTGTCATGTTGTGCGAGGGGCTGG 503
QY 510 GTTCAACACCGTGTCCCGCACGCTGGAGCGCGGGTTCAACAGCAGCAGCGGCTGACCTT 569
Db 504 GTTCTTACCGTGTCCCGCAAGTGTAGACGAGGGTTCAAGAGCGCGAAGCGGTGACCAT 563
QY 570 GACCGTGACGAGGAGAGCAGGTGCGAAGTGGAGCAGGATCTCAAGCGCGCTTCA 629
Db 564 ATCGCGCTGGAGGGGAGCAGGTGCGAAGTGGAGCAGGATCTCGAAGCGCTCTTCAG 623
QY 630 GTGGGCTGACACCCCGCTGTGATCCCGCAGATGCGAGAGCTTGGCATCAAGATTA 689
Db 624 GTGGGCTGACACCCCGCTGTGATCCCGCAGATGCGAGAGCTTGGCATCAAGATTA 683
QY 690 GAACGAAGCAGCAGGAGATCGTTGCGCTCGTTAAGATCAAA 730
Db 684 AAACGAGCTGCGCAGATCGTTGCGCTCGTTAAGACCAA 724
```

```
RESULT 8
CD439415
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 600)
Zea mays
Zea mays
EST.
CD439415.1 GI:31355058
```

```
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sequencing of the maize endospERM ESTs
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.
Unpublished
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.
```

FEATURES

Location/Qualifiers

```
source
1. 600
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="EndospERM of 7-23DAP"
/clone_lib="EndospERM 5"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
```

BASE COUNT 139 a 168 c 207 g 86 t

Query Match 55.9%; Score 419.2; DB 14; Length 600;
Best Local Similarity 85.3%; Pred. No. 3.1e-85;
Matches 512; Conservative 0; Mismatches 13; Indels 75; Gaps 1;

```
QY 97 ATCAAACTGCACGACCATAAAGGATCTTCCAGCCCGTCTGCTCCACCGGAGAAAG 156
Db 1 ATCAAACTGCACGACCATAAAGGATCTTCCACGAGCTGCCACCGGAGAAAG 60
QY 157 GTCCCGGAGCTATGTTCTACACAGAACTGAAAACAGAGCTCCATCACTCGCTGCC 216
Db 61 GTCCCGGAGCTATGTTCTACACAGAGCTCAAACTAGACACAGCTCCATCACTCGCTGCC 120
QY 217 ATACGATGGAACAACCTGTACTCTGTGGCTTTCAGAGCCCGGGCGGGTGTGTGGGAG 276
Db 121 ATACGATGGAACAACCTGTACTCTGTGGCTTTCAGAGCCCGGGCGGGTGTGTGGGAG 180
QY 277 TTCCGAAGGAGCGGCGACACCCACCTCTCGCGGCAACCCACAGTGGTTCGGCTTCGCG 336
Db 181 TTCCGAAGGAGCGGCGACACCCACCTCTCGCGGCAACCCACAGTGGTTCGGCTTCGCG 240
QY 337 GCGAGTACAGGAGCTCATCTGCGAAGAGGTCTGAGAGCCGTCACTATGAGCCCGCGCC 396
Db 241 GCGAGTACCATTAATTTTCATCGCAACAGAGGTCTGAGAGCCGTCACTATGAGCCCGCGCC 300
QY 397 GAATGACAGGCGCGTCAACGACCTGCGGAGAGAGAGAG----- 438
Db 301 GAATGACAGGCGCGTCAACGACCTGCGGAGAGAGAGAGAGATGGCGACACTGGAGGAG 360
QY 439 -----GCG 441
Db 361 GAGGAGGTGCAGATGCAGATCGGAGGCGCGTGTATCTGCGCGCGCGCGCAGCG 420
QY 442 GCTGACCCACAGGCGCGACACGAGAGAGCTGTGTAAGCTGTGCTCATGTGTGCGAG 501
Db 421 GCTGACCCACAGGCGCGACACGAGAGAGCTGTGTAAGCTGTGTAAGCTGTGCTCATGTGTGCGAG 480
QY 502 GGGCTGCGGTTCAACACCGTGTCCCGCAGCTGAGCGCGGTTTCAACAGCCAGCACCGG 561
Db 481 GGGCTGCGGTTCAACACCGTGTCCCGCAGCTGAGCGCGGTTTCAACAGCCAGCACCGG 540
QY 562 GTGACCTTGCAGCTGACGCGGAGAGCAGGTGAGAGAGTGGAGCAGGATCTCCAAGCG 621
Db 541 GTGACCTTGCAGCTGACGCGGAGAGCAGGTGAGAGAGTGGAGCAGGATCTCCAAGCG 600
```

RESULT 9
BF481680

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sorghum propinquum
Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 562)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
L.H.

BF481680.1 GI:11552501
EST.

ORGANISM

REFERENCE
AUTHORS

An EST database from Sorghum: floral-induced meristems
 Unpublished
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu
 Sequences have been trimmed to exclude PolyA, vector and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20.
 Seq primer: JEN REV
 High quality sequence stop: 498
 POLYA-No.
 Location/Qualifiers
 1..562
 /organism="Sorghum propinquum"
 /mol_type="mRNA"
 /db_xref="taxon:132711"
 /clone_lib="Floral-Induced Meristem 1 (FM1)"
 /note="Organ: Floral-induced meristems; Vector:
 pBluescript II from lambda Zap II; Site 1: XhoI; Site 2:
 EcoRI; mature plants were placed in a growth chamber for
 15 days with 16 hr darkness and 8 hr light (flowering is
 induced by short-day conditions); 16 days after being
 returned to the greenhouse under natural long days during
 late April/early May, meristems were harvested. The
 library was made from poly-A RNA in the cloning vector
 lambda Zap II. Clones to be sequenced were prepared by
 mass excision."
 151 a 160 c 154 g 97 t
 BASE COUNT
 ORIGIN
 Query Match 49.4%; Score 370.8; DB 10; Length 562;
 Best Local Similarity 90.4%; Pred. No. 3.2e-74;
 Matches 396; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
 QY 1 ATGAAAGAAAGTCCCAAGTTCTACTGAATCTCCCGGTGGAGCGCACTACCT 60
 Db 87 AAGAAAAAATAGTACCAAGTTCTACTGAAACCTTCCCGGTGGAGCGTGAAGT 146
 QY 61 TACAGCGCTTCATCGCTCGGTCCGGAAGAGCTGATCAACACTGCACCGACCAATAA 120
 Db 147 TACGCTCTTCATCGCGCGGTACGAAAGATGTGTTCAATATCTGCACCGCAATAA 206
 QY 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAAAGTCCCGGAGTATGTTCTACACA 180
 Db 207 GGCATCTTCCAGCCTGTCTCGCGCGGAGAGAGTCCCGGAGTCTGTTCTACACC 266
 QY 181 GAACCTGAAACTAGGACCACTCCATCAGCTCGCCATACGATCGGCAACCTGTACCTC 240
 Db 267 CAGCTCAAAACCAAGACCACTCCATCAGCTCGCCATACGATCGGCAACCTGTACCTC 326
 QY 241 GTGGCTTTCAGAACCCCGCGGGGTGTGGTGGAGTTCCGCAAGAGCGGACACCCAC 300
 Db 327 GTCGCTTTCAGAACCCCGCGGGTGTGGTGGAGTTCCGCAAGAGCGGACACCCAC 386
 QY 301 CTCCTCGGCGCAACCCCGAGTGGCTTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
 Db 387 CTCCTCGACGCAACCCCGAGTGGCTTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 446
 QY 361 AACAGGGTCTGAGACCGTCACTTGGCCCGCGGAAATGACAGGCGGTCAACGAC 420
 Db 447 AATAAGGGCTTGGAGCGGTCACTTGGCCCGGTGGCCCGGTGGCCCGGTCAACGAC 506
 QY 421 CTGGCGAAGAAAGAAG 438
 Db 507 CTGGCGAAGAACGACG 524
 RESULT 10
 CC332989/c
 LOCUS CC332989 846 bp DNA linear GSS 16-MAY-2003
 DEFINITION OCTAH31TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMWBMA0388F14,
 genomic survey sequence.
 ACCESSION CC332989
 VERSION CC332989.1 GI:30802272
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 846)
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick
 A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek
 R.W., Nunberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..846
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMA0388F14"
 /note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 160 a 253 c 226 g 207 t
 BASE COUNT
 ORIGIN
 Query Match 49.3%; Score 369.6; DB 29; Length 846;
 Best Local Similarity 78.3%; Pred. No. 6.6e-74;
 Matches 481; Conservative 0; Mismatches 79; Indels 54; Gaps 1;
 QY 171 GTTCTACACAGAACTGAAACTAGGACAGCTCCATCAGCTCGCCATACCATGGACAA 230
 Db 837 GTTCTACACGAGCTCAAACAGAGACAGGTCCATCAGCTCGCCATACGTATGGACAA 778
 QY 231 CCTTACTCTGTGGCTTCAGGACCCCGGGGGGTGTGTGGAGTTCGGCAAGGACGG 290
 Db 777 CCTTACTCTGTGGCTTCAGGACCCCGGGGGGTGTGTGGAGTTCGGCAAGGACGG 718
 QY 291 CGACACCACTCTCGCGGACAAACCCAGGTGCTCGGCTTCGGCGGAGTACCAGGA 350
 Db 717 CGACACCACTCTCTCGACGACAAAGTGGCTCGGCTTCGGCGGAGTACCAGGA 658
 QY 351 CCTCATCGGCAACAGGGTTCGGAGACCGTCCATGGGCGCGCCGCAAAATGACAGGGC 410
 Db 657 CCTCATCGGCAAGGGCTTCGGAGACCGTCCATGGGCGCGTCCGCAAAATGACAGGGC 598
 QY 411 CGTCAACGACCTGCGGAAGAGAGAGAG-----438
 Db 597 CGTCAACTACTCTGGGAG 538
 QY 439 -----GGGCTGACCCACAGCCGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
 Db 537 GGAGCTGCTGCTGCTGAGGCGAGCGGTGACCCCAAGCCGAGAGAGAGAGAGAGAGAGAG 478
 QY 477 GAAGCTGCTGCTGCTGCTGAGGCGGCTTCGGGTTCACACCGGTTCGCCACCGTGA 536
 Db 477 GAAGCTGCTGCTGCTGCTGAGGCGGCTTCGGGTTCCTTACCGGTTCGCCCAAGGTAGA 418
 QY 537 CGCGGGTTCAACAGCCGAGCGGGGTGACCTTACCGGTGACGCGGAGAGAGAGAGAGAGAG 596
 Db 417 CGAGGGTTCAAGAGCGCGAAGCGGTGACCATATTCGGCGCTGGAGGGGAGAGAGAGAGAG 358

Qy	597	GAAGTGGACACAGGATCTCCAAAGCGCGCTTCAGATGGGTGACACCCACCGCTGTGAT	656
Db	357	GAATGGGACAGATCTCGAAGCCGTCTTCAGTGGGCCGTGACCCGACCGCTGAGAT	298
Qy	657	CCCCACATGCAGAAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGATCGTTGCGCT	716
Db	297	CCCCGACATGAAGGATCTTGGCATCAAGATAAATAACGACAGCTGGCGAGATCGTTGCGCT	238
Qy	717	CGTTAAGAAATCAAA	730
Db	237	CGTTAAGGACCAAA	224

RESULT 11					
CD448302/c					
LOCUS	CD448302	672 bp	mRNA	linear	EST 03-JUN-2003
DEFINITION	EKO07D2305H08.g	Endosperm	6 Zea mays	cDNA,	mRNA sequence.

VERSION	CD448302.1	GI:31363947
KEYWORDS	EST.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	

AUTHORS Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.
TITLE Sequencing of the maize endosperm ESTs
JOURNAL Unpublished
COMMENT Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seg primer: T7.

```

seq primer: 17
Location/Qualifiers
1..672
  /organism="Zea mays"
  /mol_type="mRNA"
  /cultivar="W22"
  /db_xref="taxon:4577"
  /tissue_type="Endosperm of 7-23 DAP"
  /clone_lib="Endosperm 6"
  /note="vector: pak-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT
106 a 212 c 176 g 178 t

```

Query Match	46.4%	Score 348;	DB 14;	Length 672;
Best Local Similarity	85.2%	Pred. No. 5.1e-69;		
Matches 433;	Conservative	0;	Mismatches 0;	Indels 75; Gaps 1;

312	CAACCCAGTGCGCTTCGGCTTCGGCGGAGGTA	CGAGACCTCATCGGCAACAAGGGTCT	371
672	CAACCCAGTGCGCTTCGGCTTCGGCGGAGGTAC	CGAGACCTCATCGGCAACAAGGGTCT	613
372	GGAGACCGTCAACCATGGGCGCGCGGCGGAAAT	CACGAGGCCCTCAACGACCTGGCGCAAGAA	431
612	GGAGACCGTCAACCATGGGCGCGCGGCGGAAAT	CACGAGGCCCTCAACGACCTGGCGCAAGAA	553
432	GAAGAAG-----	-----	438
552	GAAGAAGATGGCGACCTGGAGGAGGAGGAGGT	GCAGATGCAGATGCCGAGGC	493
439	-----	GGGGCTGACCCACAGGCCGACACGAAGACGACTGGT	476
492	CGCTGATCTTGGCGCGCGGCGAGCGGGCTGACCC	CAGGCCGACACGAAGACGACTGGT	433
477	GAAGCTGGTGGTTCATGTTGTGCGAGGGGCTCG	CGGTTCAACACCGTGTCCCGACCGGTGGA	536

Db	432	GAAGCTGGTGTCAATGTGTGCGAGGGGCTGGGTTCAACACCGTGTCCCGCACGGTGA	373
Qy	537	CGCGGGGTTCAACACGACGACACGCGGGGTGACCTTTGACCGTGACGCGAGGGGAAGCAGGTGCA	596
Db	372	CGCGGGGTTCAACAGCCAGCACGCGGGGTGACCTTTGACCGTGACGCGAGGGGAAGCAGGTGCA	313
Qy	597	GAAGTGGGACAGGATCTTCAAGCGGGCCCTTCGAGTGGGCTGACCAACCCACCGGTGTGAT	656
Db	312	GAAGTGGGACAGGATCTTCAAGCGGGCCCTTCGAGTGGGCTGACCAACCCACCGGTGTGAT	253
Qy	657	CCCCGACATGCAGAAAGCTTGGCATCAAGGATAAGAACGAAGCAGCAGGAGATCGTTGCGCT	716
Db	252	CCCCGACATGCAGAAAGCTTGGCATCAAGGATAAGAACGAAGCAGCAGGAGATCGTTGCGCT	193
Qy	717	CGTTAAGAAATCAAACTACTGCCGTGCC	744
Db	192	CGTTAAGAAATCAAACTACTGCCGTGCC	165

RESULT_12					
CD448545/c					
LOCUS	CD448545	695 bp	mRNA	linear	EST 03-JUN-2003
DEFINITION	EX072303A09..b Endosperm_6 Zea mays cDNA, mRNA sequence.				
ACCESSION	CD448545				
VERSION	CD448545.1 GI:31364190				
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.
TITLE
Sequencing of the maize endosperm ESTs
JOURNAL
Unpublished
COMMENT
Contact: Lai, Jinsheng
Dr. Joachim Messing's lab
Waksman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735

```

FEATURES
source
seq primer: 13:
Location/Qualifiers
1..695
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23 DAP"
/clone_lib="Endosperm 6"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
120 a 214 c 176 g 185 t
BASE COUNT
ORIGIN

```

Query Match.	45.3%;	Score 340;	DB 14;	Length 695;
Best local Similarity	85.0%;	Pred. No. 3.4e-67;		
Matches 425;	Conservative 0;	Mismatches 0;	Indels 75;	Gaps 1;
QY	320	GGTGGCTCGGCTTCGGCGCAGGTACACAGACCTCATCGCACRAAGGCTCTGGAGACCG	379	
Db	695	GGTGGCTCGGCTTCGGCGCAGGTACAGGACCTCATCGCACRAAGGCTCTGGAGACCG	636	
QY	380	TCACCAATGGGCCCGCGCGAAATGACACAGGCCGTCAACGACCTGGCGAAGAAGAAG-	438	
Db	635	TCACCAATGGGCCCGCGCGAAATGACACAGGCCGTCAACGACCTGGCGAAGAAGAAGA	576	
QY	439	-----	438	
Db	575	TGCGGCACGTGAGAGAGAGAGGTGCGATGCAGATGCAGATGCCGGAGCGCGCTGCATC	516	
QY	439	-----GCGGCTGACCCACAGCGCGCGACACGAGACGACGCTGGTGAAGCTCGG	484	

Db 515 TGGCGGCGCGGACGCGGCTGACCCACAGGCGCCACACGAAAGCAAGCTGGTGAAGCTGG 456
Qy 485 TGGTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGCGGGGT 544
Db 455 TGGTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGCAGCGTGGACGCGGGGT 396
Qy 545 TCAACAGCCAGCAGCGGGGTGACCTTTCACCGTGACGCGAGGGGAAGCAGGTGCAGAAAGTGGG 604
Db 395 TCAACAGCCAGCAGCGGGGTGACCTTTCACCGTGACGCGAGGGGAAGCAGGTGCAGAAAGTGGG 336
Qy 605 ACAGGATCTTCAAGCGCGCTTCGAGTGGCTGACCAACCCACCGCTGTGATFCCCGGACA 664
Db 335 ACAGGATCTTCAAGCGCGCTTCGAGTGGCTGACCAACCCACCGCTGTGATFCCCGGACA 276
Qy 665 TGCAGAAGCTTGGCATCAGGATAGACGAGGAGCAGGAGGATCGTGGCTCGTTAAGA 724
Db 275 TGCAGAAGCTTGGCATCAGGATAGACGAGGAGCAGGAGGATCGTGGCTCGTTAAGA 216
Qy 725 ATCAAACTACTGCGGCTGCC 744
Db 215 ATCAAACTACTGCGGCTGCC 196

RESULT 13
T18690
LOCUS
DEFINITION
5C04F01-T7 membrane-free polysomes from endosperm Zea mays cDNA
clone 5C04F01 5' end similar to ribosome inactivating protein, mRNA
sequence.
T18690
T18690.1 GI:485620
EST.
Ze mays
Ze mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,
Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J. and
Larkins, B.
Partial sequencing and mapping of clones from two maize cDNA
libraries
Plant Mol. Biol. 26, 1085-1101 (1994)
95111093
7811968
Contact: The Maize cDNA Project

Helentjaris TG (primary contact)
Dept. of Plant Sciences
University of Arizona
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721
ph: 602-6218-746
fax: 602-621-7186
E-mail: helnjaris@ccit.arizona.edu

Chris Baysdorfer
Department of Biological Sciences, School of Science
California State University, Hayward
Hayward, CA 94542
ph: 510-881-3459
fax: 510-727-2035
E-mail: cbaysdor@sl.csu Hayward.edu

Rob Ferl
Interdisciplinary Center for Biotechnology Research
DNA Sequencing Core
University of Florida
P.O. Box 100695
Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072

E-mail: roberl@nervm.nerdc.ufl.edu
Seq primer: T7
Location/Qualifiers
1. 366
/organism="Zea mays"
/mol_type="mRNA"
/strain="W64A2"
/db_xref="taxon:4577"
/clone="5C04F01"
/lab_host="DH10B"
/clone_lib="membrane-free polysomes from endosperm"
/note="Vector: ZipLox; Site 1: SalI; Site 2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a
NotI oligo- dT oligomer and then adding the second strand
to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI
adaptors were added to the ends, the ds-cDNAs were then
digested with NotI and size-selected. These were
directionally-cloned into the ZipLox phage vector, excised
as plasmids, and then individually analyzed."
BASE COUNT 80 a 117 c 110 g 56 t 3 others
ORIGIN

Query Match 44.9%; Score 336.6; DB 14; Length 366;
Best Local Similarity 98.3%; Pred. No. 1.7e-66;
Matches 350; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 37 CCGTGGAGGACGGAATACCTTACAGCGCTTCATCGGTCGGTCCGGAACACGTG 96
Db 12 CCGTGGAGGACG- GAATACCTTACAGCGCTTCATCGGTCGGTCCGGAACACGTG 70
Qy 97 ATCAAACTACTGACCGACCATAAAGGATCTTCCAGCCCGTCTCCACCGGAGAGAAG 156
Db 71 ATCAAACTACTGACCGACCATAAAGGATCTTCCAGCCCGTCTCCACCGGAGAGAAG 130
Qy 157 GTCCCGGAGCTATGGTTCTACACAGAACTGAAACCTAGGACAGCTCCATCAGCTCGCC 216
Db 131 GTCCCGGAGCTATGGTTCTACACAGAGCTCAAACTAGGACAGCTCCATCAGCTCGCC 190
Qy 217 ATAGCATGGAACCTGTACTCTGTGGCTTCAGGACCCCGGGGGGTGTGGGAG 276
Db 191 ATAGCATGGAACCTGTACTCTGTGGCTTCAGGACCCCGGGGGGTGTGGGAG 250
Qy 277 TTGCGCAAGGACGCGACACCCACCTCTCGCGGACACACCCAGGTGCTCGGCTCGGC 336
Db 251 TTGCGCAAGGACGCGGACACCTCTCTCGCGGACACACCCAGGTGCTCGGCTCGGC 310
Qy 337 GGCAGGTACGAGGACCTCATCGGCAACAAGGTTCTGGAGACCGTCCATCGGCGC 392
Db 311 GGCAGGTACGAGGACCTCATCGGCAACAAGGTTCTGGAGACCGTCCATCGGCGC 366

RESULT 14
A1667697/c
LOCUS
DEFINITION
605026A04.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence.
ACCESSION
A1667697
VERSION
A1667697.1 GI:4826069
KEYWORDS
EST.
SOURCE
Ze mays
ORGANISM
Ze mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 436)
AUTHORS
Maize ESTs from various cDNA libraries sequenced at Stanford
Walbot, V.
TITLE
University
JOURNAL
Unpublished
COMMENT
Contact: Walbot V
Department of Biological Sciences
Stanford University

Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605004 row: F column: 08.

FEATURES
SOURCE

```

1. .436
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="Ohio43"
/db xref="taxon:4577"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/note="Organ: Kernel; Vector: pAD-GAL4-2; Site 1: EGOR1; Site 2: XhoI; Kernel endosperm cDNA library from Schmidt lab"
lab"

```

BASE COUNT	74 a	135 c	121 a	106 t
100	100	100	100	100
101	101	101	101	101
102	102	102	102	102
103	103	103	103	103
104	104	104	104	104
105	105	105	105	105
106	106	106	106	106
107	107	107	107	107
108	108	108	108	108
109	109	109	109	109
110	110	110	110	110
111	111	111	111	111
112	112	112	112	112
113	113	113	113	113
114	114	114	114	114
115	115	115	115	115
116	116	116	116	116
117	117	117	117	117
118	118	118	118	118
119	119	119	119	119
120	120	120	120	120
121	121	121	121	121
122	122	122	122	122
123	123	123	123	123
124	124	124	124	124
125	125	125	125	125
126	126	126	126	126
127	127	127	127	127
128	128	128	128	128
129	129	129	129	129
130	130	130	130	130
131	131	131	131	131
132	132	132	132	132
133	133	133	133	133
134	134	134	134	134
135	135	135	135	135
136	136	136	136	136
137	137	137	137	137
138	138	138	138	138
139	139	139	139	139
140	140	140	140	140
141	141	141	141	141
142	142	142	142	142
143	143	143	143	143
144	144	144	144	144
145	145	145	145	145
146	146	146	146	146
147	147	147	147	147
148	148	148	148	148
149	149	149	149	149
150	150	150	150	150
151	151	151	151	151
152	152	152	152	152
153	153	153	153	153
154	154	154	154	154
155	155	155	155	155
156	156	156	156	156
157	157	157	157	157
158	158	158	158	158
159	159	159	159	159
160	160	160	160	160
161	161	161	161	161
162	162	162	162	162
163	163	163	163	163
164	164	164	164	164
165	165	165	165	165
166	166	166	166	166
167	167	167	167	167
168	168	168	168	168
169	169	169	169	169
170	170	170	170	170
171	171	171	171	171
172	172	172	172	172
173	173	173	173	173
174	174	174	174	174
175	175	175	175	175
176	176	176	176	176
177	177	17		

BASE COUNT	74 a	135 c	121 g	106 t
ORIGIN				
Query Match		40.8%	Score 306;	DB 9; Length 436;
Best Local Similarity		100.0%;	Pred. No. 1.7e-59;	

```
0:      best local similarity    100.0%, Freq. no. 1.7e-39,  
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
0:      428 GAGGCTGTCCCCACGGCGGCACACCAACGATCTGCTGCTTACTGCTTCAC 498
```

Qy	439	GC	GCTGACCCACAGGCCGACACG	AGCAGCAAGCTGGTGAAGCTGGTGGT	CATGGTGTGC	498
Dh	425	GC	GGGTGACCCACAGGCCGACACG	AGCAGCAAGCTGGTGAAGCTGGTGGT	ATGGTGTGC	366

Db	425	GGGCTGACCCACAGGCCGACACGAAAGCAAGCTGGTGAAGTGGTGGTTCATGGTGTGC	366
Ov	499	GAGGGGCTGCGGTTCAACACCGTGTCCGCAACGCTGGACCGGGGTTCAACAGCCAGCAC	558

Qy	499	GAGGGGTGCGGTTCAACACCGTGTCCGCGACGCTGGACGGGGTTCAACAGCCAGCAC	558
Db	365	GAGGGGTGCGGTTCAACACCGTGTCCGCGACGCTGGACGGGGTTCAACAGCCAGCAC	306

Db	365	GAGGGGTGCGGTTCAACACCGTGTCCCGACCGTGGACGCGGGGTTCAACAGCCAGCAC
Qy	559	GGCGTGACCTTGACCGTGACGCGAGGGGAAGCAGGTGCAGAAAGTGGGACAGGATCTCCAAG

Qy	559	GGGGTGACCTTGACCTGTCACGCGAGGGGAGCAGGTGCGAAGTGGGACAGGATCTCCAG
Db	305	GGGGTGACCTTGACCTGTCACGCGAGGGGAGCAGGTGCGAAGTGGGACAGGATCTCCAG

Db	305	GGGGTGACCTTGACCTGACGCGAGGGGAAGCAGGTGCAGAAAGTGGGACAGGAATCTCCAG
Qy	619	GGGGCTTCGAGTGGGTGACACCCACCGCTGTATCCCCGACATGCAGAGAAGCTTGGC

QY	619	CGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCCGACATGCAGAGCTTGC	678
Db	245	CGCGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCCGACATGCAGAGCTTGC	186

DB	245	GC	CGCCCTTCGAGTGGGGCTGACCA	ATCCACCGCTGTGATCCCCCGCATGACAGAACTTGC	188
Qy	679	AT	CAAGGNTAAGACGAACGACGAGGATCGTTGCGCTCGTTAAGAAATCAAACTACTGCC	738	

QY 679 ATCAAGGAAAGAGACGAACAGCAGGAGATCGTTCGGCTCGTAAAGHICAAACACCTGCC 738

Db 185 ATCAAGGATAGAACGAACAGCAGGAGATCGTTCGGCTCGTAAAGATCAAACTACTGCC 126

[illegible]

Db 125 GCTGCC 120

RESULT 15

AI664942/c
LOCUS AI664942 573 bp mRNA linear EST 02-FEB-2000
DEFINITION 605004F08.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
cDNA, mRNA sequence.

ACCESSION
AI664942

VERSION AI664942.1 GI:4775939

KEYWORDS EST.

SOURCE

ORGANISM	Zea mays
REFERENCE	1 (bases 1 to 573)
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases

AUTHORS Walbot, V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
JOURNAL Unpublished
COMMENT Contact: Walbot V

COMMENT	CONTACT
	Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227

Tel: 650 723 2227

Search completed: October 22, 2003, 06:50:05
Job time : 2055 secs

Query Match	40.8%;	Score 306;	DB 9;	Length 573;	
Best Local Similarity	100.0%;	Pred. No. 1.8e-59;			
Matches 306;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	439	GCGGCTGACCCACAGCGCCGACACGAGACAGCAAGCTGGTGAAGCTGGTGGTCTCATCGTGTGC	498		
Db	539	GCGGCTGACCCACAGCGCCGACACGAGAGCAAGCTGGTGAAGCTGGTGGTCTCATCGTGTGC	480		
Qy	499	GAGGGGCTGGGTTCACACCGTGTCCCGCACGGTGGACGCGGGGTTCAACAGCCAGCAC	558		
Db	479	GAGGGGCTGGGTTCACACCGTGTCCCGCACGGTGGACGCGGGGTTCAACAGCCAGCAC	420		
Qy	559	GGGGTGACCTTGACCGTGACGCGGGGAAACAGGTGCAGAGTGGGACAGGATCTCCAAG	618		
Db	419	GGGGTGACCTTGACCGTGACGCGGGGAAACAGGTGCAGAGTGGGACAGGATCTCCAAG	360		
Qy	619	GCGGCCTTCAGTGGGCTGACACCCACCGCTGTGATCCCGACATGCAGAACTGTGC	678		
Db	359	GCGGCCTTCAGTGGGCTGACACCCACCGCTGTGATCCCGACATGCAGAACTGTGC	300		
Qy	679	ATCAAGGATTAAGAACGAAGCAGCGAGGATCGTTGCGCTCGTTAGAGATCAAACTACTGCC	738		
Db	299	ATCAAGGATTAAGAACGAAGCAGCGAGGATCGTTGCGCTCGTTAGAGATCAAACTACTGCC	240		
Qy	739	GCTGCC	744		
Db	239	GCTGCC	234		

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 06:15:45 ; Search time 282 Seconds
(without alignments)
7132.449 Million cell updates/sec

Title: US-09-978-273-2
Perfect score: 750
Sequence: 1 atgaagaagaatagtgccaaa.....ctactgcgcgtgctaataa 750

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 segs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750	100.0	750	10	US-09-978-273-2
2	656	87.5	909	10	US-09-978-273-1
3	438	58.4	444	10	US-09-978-273-3
4	307.4	41.0	354	10	US-09-978-273-4
5	113.8	15.2	240	9	US-09-294-093B-1275
6	77.6	10.3	846	12	US-10-127-890-12
7	55.6	7.4	2340	9	US-09-815-242-7995
8	55.4	7.4	1299	14	US-10-156-761-1179
9	55.4	7.4	9025608	14	US-10-156-761-1
10	54.4	7.3	4725	14	US-10-205-032-17
11	54.4	7.3	60196	14	US-10-205-032-1
12	52	6.9	5487	14	US-10-156-761-2499
13	52	6.9	9025608	14	US-10-156-761-1
14	51.8	6.9	1377	9	US-09-846-590B-17
15	51.2	6.8	11238	14	US-10-205-032-15
16	50.2	6.7	1098	14	US-10-156-761-5369

17	50	6.7	18438	14	US-10-156-761-2886	Sequence 2886, Ap	
18	50	6.7	125746	14	US-10-156-761-15102	Sequence 15102, A	
c	19	49.8	6.6	1434	12	US-10-271-889-3	Sequence 3, Appli
	20	49.8	6.6	1815	14	US-10-156-761-5249	Sequence 5249, Ap
	21	49.8	6.6	88421	10	US-09-976-059-1	Sequence 1, Appli
	22	49.4	6.6	1041	14	US-10-156-761-594	Sequence 594, App
	23	49.4	6.6	1260	14	US-10-156-761-1993	Sequence 1993, Ap
	24	49.4	6.6	1428	14	US-10-156-761-2812	Sequence 2812, Ap
	25	48.6	6.5	468	14	US-10-156-761-6877	Sequence 6877, Ap
	26	48.6	6.5	1974	14	US-10-156-761-2174	Sequence 2174, Ap
	27	48.4	6.5	1533	14	US-10-156-761-2574	Sequence 2574, Ap
	28	48.4	6.5	1608	14	US-10-168-843A-27	Sequence 27, Appl
	29	48.4	6.5	1914	14	US-10-168-843A-29	Sequence 29, Appl
	30	48.4	6.5	2493	14	US-10-168-843A-31	Sequence 31, Appl
	31	48.4	6.5	4350	14	US-10-168-843A-33	Sequence 33, Appl
	32	48.4	6.5	4653	13	US-10-101-388-2	Sequence 2, Appli
	33	48.4	6.5	8036	13	US-10-101-388-1	Sequence 1, Appli
	34	48	6.4	1263	14	US-10-156-761-1370	Sequence 1370, Ap
	35	48	6.4	1473	14	US-10-156-761-6501	Sequence 6501, Ap
	36	48	6.4	1503	14	US-10-156-761-101	Sequence 101, App
	37	47.8	6.4	738	14	US-10-156-761-5888	Sequence 5888, Ap
	38	47.8	6.4	1230	14	US-10-156-761-6774	Sequence 6774, Ap
	39	47.6	6.3	2043	14	US-10-156-761-2781	Sequence 2781, Ap
	40	47.4	6.3	639	14	US-10-156-761-1668	Sequence 1668, Ap
	41	47.4	6.3	1359	14	US-10-156-761-5437	Sequence 5437, Ap
	42	47.2	6.3	1023	14	US-10-156-761-7189	Sequence 7189, Ap
	43	47.2	6.3	1083	14	US-10-156-761-4116	Sequence 4116, Ap
	44	47.2	6.3	1662	14	US-10-156-761-3483	Sequence 3483, Ap
	45	47	6.3	1602	14	US-10-156-761-6647	Sequence 6647, Ap

ALIGNMENTS

RESULT 1
US-09-978-273-2
; Sequence 2, Application US/09978273
; Patent No. US20020138869A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Christopher
; APPLICANT: McPherson, Michael
; APPLICANT: Atkinson, Howard
; APPLICANT: Neelam, Anil
; TITLE OF INVENTION: Plant Cell Death System
; FILE REFERENCE: 9341-027
; CURRENT APPLICATION NUMBER: US/09/978, 273
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0025225.4
; PRIOR FILING DATE: 2000-10-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Initiation codon added via PCR primer
; NAME/KEY: mutation
; LOCATION: (181)..(186)
; OTHER INFORMATION: Sequence replacing removed SacI site
; NAME/KEY: misc feature
; LOCATION: (745)..(750)
; OTHER INFORMATION: Stop codons added by PCR primer
US-09-978-273-2

Query Match 100.0%; Score 750; DB 10; Length 750;
Best Local Similarity 100.0%; Pred. No. 2.2e-195;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGAAGTATAGTCCAAAGTCTACTGAATCTTCCCGTGAGGACGCACTACCCCT 60
|||||

```
Db 1 ATGAAGAAGTAGTGCACCAAGTTCACTGAATCTTCCCGTGGAGGACGGCAACTACCT 60
Qy 61 TACAGCGCTTCAATCGCGTGGTCCGAAAGACGTGATCAAAACACTGACCGACATAAA 120
Db 61 TACAGCGCTTCAATCGCGTGGTCCGAAAGACGTGATCAAAACACTGACCGACATAAA 120
Qy 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCGGAGCTATGTTCTACACA 180
Db 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCGGAGCTATGTTCTACACA 180
Qy 181 GAATGAAACTAGGACAGCTCCATCAAGCTGCCATAGCATGAGCAACCTGTACCTC 240
Db 181 GAATGAAACTAGGACAGCTCCATCAAGCTGCCATAGCATGAGCAACCTGTACCTC 240
Qy 241 GTGGGCTTACAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGACGGCGACCCAC 300
Db 241 GTGGGCTTACAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGACGGCGACCCAC 300
Qy 301 CTCTCGCGCACACCCAGGTGGTCTGGTTCGGCGGAGGTACAGGACCTCATCGC 360
Db 301 CTCTCGCGCACACCCAGGTGGTCTGGTTCGGCGGAGGTACAGGACCTCATCGC 360
Qy 361 AACAGGCTCGAGACCGTCAACATGGCGCGCGCGAAATGACAGGGCGGTCAACGAC 420
Db 361 AACAGGCTCGAGACCGTCAACATGGCGCGCGCGAAATGACAGGGCGGTCAACGAC 420
Qy 421 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAAGACGAGCTGGTGAAG 480
Db 421 CTGGCGAAGAAAGAGGCGGTGACCCACAGCGCGACACGAAGACGAGCTGGTGAAG 480
Qy 481 CTGGTGTCTATGTGTGCGAGGAGTGGCTTCAACACGCTGTCGGCGAGGTGAGCGG 540
Db 481 CTGGTGTCTATGTGTGCGAGGAGTGGCTTCAACACGCTGTCGGCGAGGTGAGCGG 540
Qy 541 GGGTTCAACAGCAGCAGCGGGTGACCTTGACCGTGAAGGAGGAGGAGGAGGAGGAG 600
Db 541 GGGTTCAACAGCAGCAGCGGGTGACCTTGACCGTGAAGGAGGAGGAGGAGGAGGAG 600
Qy 601 TGGGACAGGATCTCAAGCGGCTTCAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Db 601 TGGGACAGGATCTCAAGCGGCTTCAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Qy 661 GACATCAGAAGCTTGGCATCAAGGATAGAACGAGCAGCAGGATCGTGGCGTCGTT 720
Db 661 GACATCAGAAGCTTGGCATCAAGGATAGAACGAGCAGCAGGATCGTGGCGTCGTT 720
Qy 721 AAGAATCAAACTACTGCGCGTGCCTAATAA 750
Db 721 AAGAATCAAACTACTGCGCGTGCCTAATAA 750
```

RESULT 2

US-09-978-273-1
; Sequence 1, Application US/09978273
; Patent No. US20020138869A1

GENERAL INFORMATION:

APPLICANT: Thomas, Christopher

APPLICANT: McPherson, Michael

APPLICANT: Atkinson, Howard

APPLICANT: Neelam, Anil

TITLE OF INVENTION: Plant Cell Death System

FILE REFERENCE: 9341-027

CURRENT APPLICATION NUMBER: US/09/978,273

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 0025225.4

PRIOR FILING DATE: 2000-10-14

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 909

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

```
; NAME/KEY: misc feature
; LOCATION: (1)..(48)
; OTHER INFORMATION: N-terminal Domain
; NAME/KEY: misc feature
; LOCATION: (85)..(903)
; OTHER INFORMATION: C-terminal Domain
; NAME/KEY: misc feature
; LOCATION: (484)..(558)
; OTHER INFORMATION: Central Domain
; NAME/KEY: mutation
; LOCATION: (226)..(231)
; OTHER INFORMATION: Sequence replacing removed SacI site
; NAME/KEY: misc feature
; LOCATION: (1)..(3)
; OTHER INFORMATION: Initiation codon added via PCR primer
; NAME/KEY: misc feature
; LOCATION: (904)..(909)
; OTHER INFORMATION: Stop codons added via PCR primer
; NAME/KEY: misc feature
; LOCATION: (1)..(24)
; OTHER INFORMATION: Binding site for primer ProRIPBF
; NAME/KEY: misc feature
; LOCATION: (205)..(249)
; OTHER INFORMATION: Binding site for primer RIPSDF
; NAME/KEY: misc feature
; LOCATION: Complement((205)..(249))
; OTHER INFORMATION: Binding site for primer RIPSDF
; NAME/KEY: misc feature
; LOCATION: Complement((880)..(909))
; OTHER INFORMATION: Binding site for primer ProRIPSR
; NAME/KEY: misc feature
; LOCATION: (49)..(73)
; OTHER INFORMATION: Binding site for primer RIP1BF
; NAME/KEY: misc feature
; LOCATION: Complement((837)..(864))
; OTHER INFORMATION: Binding site for primer RIP2SR
; NAME/KEY: misc feature
; LOCATION: (463)..(579)
; OTHER INFORMATION: Binding site for primer RIPCDF spanning central
; OTHER INFORMATION: domain
; NAME/KEY: misc feature
; LOCATION: Complement((463)..(579))
; OTHER INFORMATION: Binding site for primer RIPCDR spanning central
; OTHER INFORMATION: domain
; US-09-978-273-1
```

Query Match 87.5%; Score 656; DB 10; Length 909;

Best Local Similarity 90.8%; Pred. No. 1.1e-169;

Matches 741; Conservative 0; Mismatches 0; Indels 75; Gaps 1;

```
Qy 4 AAAAGAATAGTCCCAAAAGTTCACTGAATCTTCCCGTGGAGGACGGCAACTACCTTAC 63
Db 49 AAAAGAATAGTCCCAAAAGTTCACTGAATCTTCCCGTGGAGGACGGCAACTACCTTAC 108
Qy 64 AGCGCTTCATCGCTGGTCCGAAAGACGTGATCAAACTGACCGACCATAAAGG 123
Db 109 AGCGCTTCATCGCTGGTCCGAAAGACGTGATCAAACTGACCGACCATAAAGG 168
Qy 124 ATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGGAGCTATGTTCTACACAGAA 183
Db 169 ATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGGAGCTATGTTCTACACAGAA 228
Qy 184 CTGAAAACCTAGGACCAAGCTCCATCAAGCTCGCATACGATGGACCAACTGACCTCGTG 243
Db 229 CTGAAAACCTAGGACCAAGCTCCATCAAGCTCGCATACGATGGACCAACTGACCTCGTG 288
Qy 244 GCGTTACAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGGACGGCGACACCCACCTC 303
Db 289 GCGTTACAGACCCCGCGGGGTGTGTGGAGTTCGGCAAGGACGGCGACACCCACCTC 348
Qy 304 CTCGGGCAACCCCGAGGTGGCTCGGCTTCGGCGGACGATACCGAGGACCTCATCGGCAAC 363
Db 349 CTCGGGCAACCCCGAGGTGGCTCGGCTTCGGCGGACGATACCGAGGACCTCATCGGCAAC 408
```


QY 556 CACGGGTGACCTTGACCGGTGACGAGGGAACAGAGTGCAGAAAGTGGGACAGGATCTCC 615
 Db 121 CACGGGTGACCTTGACCGGTGACGAGGGAACAGAGTGCAGAAAGTGGGACAGGATCTCC 180
 QY 616 AAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCGCATGCGAGAGCTT 675
 Db 181 AAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCGCATGCGAGAGCTT 240
 QY 676 GGATCAAGGATGAAGAACAGGAGGAGGATCGTTCGCTGTTAAGATCAAACTACT 735
 Db 241 GGATCAAGGATGAAGAACAGGAGGAGGATCGTTCGCTGTTAAGATCAAACTACT 300
 QY 736 GCGCTGCC 744
 Db 301 GCGCTGCC 309

RESULT 5
 US-09-294-093B-1275
 ; Sequence 1275, Application US/09294093B
 ; Patent No. US20010051335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalguadi, Raghunath, V.
 ; APPLICANT: Ito, Laura, Y.
 ; APPLICANT: Sherman, Bradley, K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 ; FILE REFERENCE: PL-0009 US
 ; CURRENT APPLICATION NUMBER: US/09/294,093B
 ; CURRENT FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: 60/082,567
 ; PRIOR FILING DATE: April 21, 1998
 ; NUMBER OF SEQ ID NOS: 6207
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1275
 ; LENGTH: 240
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20010051335A1 700344050H1
 US-09-294-093B-1275

Query Match 15.2%; Score 113.8; DB 9; Length 240;
 Best Local Similarity 87.9%; Pred. No. 1.7e-21;
 Matches 124; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGCAGAAAGTTCACCTGAAATCTTCCCGTGAGGAGCGGAACCTACCCCT 60
 Db 100 AAGAAAATATAGTGCCAAAGTTCACCGAAACCTTCCCGTTGAGGACACGGCCTACCCCT 159
 QY 61 TACAGCGCTTCATCGCGTGGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 120
 Db 160 TACAGCGCTTCATCACTCCGTCGGAAGAGCGTGATCAAACTGCACCAACCATACA 219
 QY 121 GGCATCTCCAGCCGCTGCTG 141
 Db 220 GGCATCTCCAGCCGCTGCTG 240

RESULT 6
 US-10-127-890-12
 ; Sequence 12, Application US/10127890
 ; Publication No. US20030166196A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; Studnika, Gary M.
 ; Carroll, Stephen F.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; Proteins
 ; NUMBER OF SEQUENCES: 173
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: McAndrews, Held & Malloy, Ltd.
 ; STREET: 500 West Madison Street, 34th floor

CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/10/127,890
 APPLICATION NUMBER: US/10/127,890
 FILING DATE: 23-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70-P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 12:
 LENGTH: 846 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-10-127-890-12

Query Match 10.3%; Score 77.6; DB 12; Length 846;
 Best Local Similarity 51.2%; Pred. No. 1.6e-11;
 Matches 309; Conservative 0; Mismatches 259; Indels 36; Gaps 4;

QY 15 GCCTAGTTTCACTGAAATCTTCCCGTGAGGAGCGGAACCTACCTTACAGCGCTTCAT 74
 Db 33 GCGGCTCTTTCACCGGACGTTCAAGTCCAGGCCAGTCCGCGGACTAGCCACCTTCAT 92
 QY 75 CCGCTCGTCCGGAAGAGCTGATCAA-----ACACTGACGACCACTAAAGGATCTT 128
 Db 93 CCGCGGATCCCGCAACAAGCTCCGCAACCGCGGCACTTCTCCCAACCGCCCGCTGT 152
 QY 129 CCAGCCCGTGTCTGCCACCGGAGAAAGTCCCGGAGCTATGTTCTACACAGAACTGAA 188
 Db 153 GCGCGGCTCGAGCCCAACGTCCTCCCGGAGAGTGTTCACGTCGTCTCAAGGCCTC 212
 QY 189 AACTAGGACAGCTCCATCAGCTCGCATAGCATGGAACCTGTACTCTGTGGGCTT 248
 Db 213 GCGGACCAAGCGCGGCTCAAGTCCGCTGCGGACCAACATCTACTTGGAGGCTT 272
 QY 249 CAGGACCCCGGCGGCTGTGTTGGAGTTCGGCAAGGACGCGGACACCACTCTCTCG 308
 Db 273 CAAGAGCAGCAGCACTGTGTGGAGCT-----CACCCCGGCTCAT 317
 QY 309 CGACAAACCCAGTGGCTTCGCGGAGAGTACAGGACCTCATCGGCAACAAGG 368
 Db 318 CCGCGGCGCCTACGTGCGGTTGCGGGGACCTTACCGGACCTCTCTCGGACACCGA 377
 QY 369 TCTGGAGACCGTCACTACATGGGCGCG-----GCCGAATGACAGGCGGCTCAA 416

Db 378 CAAGCTAACCAAGTCTCGGCCGACACGACGCTCGCGGACGCGGTGACCGGCTCCA 437
QY 417 CGACCTGGCGAAGAGAGGCGGTGACCCACAGCGCCGACACAGAGAGCAAGCTGGT 476
Db 438 CGGGCGACCAAGCCGACAGGCTCGGCGCCGAAACAGCAGCAGCGGAGGAGCGGT 497
QY 477 ---GAAGCTGGTGTATGTTGTCGAGAGGCGTCCGTTCAACACCGTGTCCGACGGT 533
Db 498 GACGACGCTGGTCTCATGTGTGAACAGAGGCCACCGGTTCCAGACGGTGTCTGGGTTCTG 557
QY 534 GAGCGCGGGGTTCAACAGCAGCAGCGGGTGACCTTACCGTGACGCGAGGGAGCAGGT 593
Db 558 GGGCGGGTGTCTGACCCCAAGCGGTGGAGAAAGAGCGGGAAGATCGGCAATGAGAT 617
QY 594 GCAG 597
Db 618 GAAG 621

RESULT 7

US-09-815-242-7995
; Sequence 7995, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7995
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2340)
US-09-815-242-7995

Query Match 7.4%; Score 55.6; DB 9; Length 2340;
Best Local Similarity 44.5%; Pred. No. 2e-05;
Matches 220; Conservative 0; Mismatches 274; Indels 0; Gaps 0;
QY 66 CGCCTTATCGCTCGGTCCGGAAGACGTGATCAACACTGACCGACCATAAAGGAT 125
Db 1542 CGGCCTCAACTCGACGCTGGCGGAGAACATCGTCGGCACCGCGACGCGCAACGAGCGTT 1601
QY 126 TTCCAGCCCGTCTGCTCCACCGGAGAGAGGTCCCGGAGCTATGTTCTACACAACT 185

Db 1602 CCGCACCCCGCAGAGCTCAAGAAAGTCAAGCCGCTCGGCGAAAAGACCTTCGAGCAAGC 1661
QY 186 GAAACTAGGACAGCTCCATCAGCTCGCCATACGATAGCATGGACAACTGTACCTCGTGGG 245
Db 1662 CGCGGGTCTCTCCGCGTATGAACCGGCGACAAACCGCTGGAGCGCTCGGCGGTGCAACC 1721
QY 246 CTTACAGACCCCGCGGGGGTGTGTGGAGTTTCGGAAGACGCGGACACACCCACCTCCT 305
Db 1722 GGAGACTATCCGCTGGTCAGCGCATCGCGCCGACACCGAGCGGACATCCGCTCGCT 1781
QY 306 CGCGGACACCCAGTGGCTCGGCTTCGGCGGACAGTACAGGACCTCATCGGCAACAA 365
Db 1782 GATCGGCGACTCGGCGCTTCTCAAGCGCTTCGACCGGAAAGATTCCACGACGAGACCTT 1841
QY 366 GGTCTCGGAGACCGTCAACCATGGCGCGCGGAAATGACAGGCGGTCAACGACCTGGC 425
Db 1842 CGGCTTGGCGACCGTCAACGACATCTCAAGGAACTCGACAGCCCGCGCGACCGCG 1901
QY 426 GAAGAAAGAAAGCGGCTGACCCAGCGCGACAGAAAGCAAGCTGGTGAAGCTGGT 485
Db 1902 TCCGGAGTTCAAGACCGCAGAAATTCAGGAAGCGCTCGAGAGCTCAAGACCTCAAGCC 1961
QY 486 GGTCTATGGTTCGAGGGGCTCGGTTCAACACCGTGTCCGACGAGTGAACCGGGTT 545
Db 1962 GGGCATGGTCTCGAGGGCGTGGTGACCAACGTCACCAACTTCGGGCGGTTCTGTCGACAT 2021
QY 546 CAACAGCGACGACG 559
Db 2022 CGCGTCCACAGG 2035

RESULT 8

US-10-156-761-1179
; Sequence 1179, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1179
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1299)
US-10-156-761-1179

Query Match 7.4%; Score 55.4; DB 14; Length 1299;
Best Local Similarity 46.2%; Pred. No. 2.1e-05;
Matches 222; Conservative 0; Mismatches 256; Indels 3; Gaps 1;
QY 198 CAGCTTCATCAGCTCGCCATACGATGACAACTGTACTCTGTGGGTTTCAGGACCCC 257
Db 522 CATCTTCTACAGGGCGGACCCACCAACAGATCGTCCCGGCGCTCGACTACTCTCAA 581
QY 258 GGGCGGGTGTGTGGAGTTTCGGAAGACGCGGACACCCACCTCTCGGCGCAACCC 317
Db 582 GAGCCAGGCAAGAAAGATCTACTGTGCGAGCGACTACGTCTTCCCGCGCACCGC 641

318	QY	CAGTGGCTCGGCTTCGGCGGAGGTA	CAGGA	CTCA	TCGGCA	ACAAGG	TCTCGAGAC	377
642	Db	CAACAAGATCATCAAGGCGTACGCGAAGCCAA	CGGCAT	ACGGTCT	GGCGAGGACTA			701
378	QY	CGTCACCATGGCGCGCGGAAATGAC	CAGGCGCTCA	CGACCTTGGCGA	GAAGA	GA	GA	437
702	Db	CGCGCGTGGGCTCCACCGAGTT	CAGCAGATGCCAACAA	--GGTGA	AGCGCGCCAA			758
438	QY	GGCGGCTGACCCACAGGCGCGAC	CGAAGAGCAAGCTGGTGA	AGCTGGTGGT	CATCGTGTG			497
759	Db	GGCGACGCGGTCTTCAACAGCTCA	ACGGCGACTCA	AGTGGCCTCTTCA	AGGAGTA			818
498	QY	CGAGGGGTGCGGTTCAACACG	TTCGCGACG	TGAGCGGGTTC	ACAGCCAGCA			557
819	Db	CAAGTCGCGCGCGCTGACCGCA	AGAGCATGCGGTCG	TCTCGTGT	CGATCGCGAGA			878
558	QY	CGGGGTGACCTTGACCGTGA	CGCAGGGGAACAGGTG	CAGAAGTGGG	CAGGATCTCCA			617
879	Db	AGAGTCAAGTCGATCGGATCG	CAGTA	CGTGGCGGCGAGT	GACGGCTTGGAACTACTA			938
618	QY	GGCGGCGCTTCAGTGGGTGAC	CAACCCACCGCTGTGAT	CCCCGACATG	SCAGAGCTTGG			677
939	Db	CCAGACCACCCGGCGGCGGA	CAACCAAGTT	CGTGAAGGCT	CAAGGCCAAGTACGG			998
678	QY	C	678					
999	Db	C	999					

```

RESULT 9
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

```

Db	1481296	CAACAAGATCATCAAGGCGTACGGAAGGCCAACGGCATGACGGTGTGGCGAGGACTA	1481355
Qy	378	CGTCACCATGGCGCGCCGAATGACCAAGGCCGTCAACGACTGGCGAAGAAGAA	437
Db	1481356	CGCGCCCTGGGTCCACCGAGTTCAGCATGCGCAACAA---GGTGAAGCGGCGCAA	1481412
Qy	438	GGCGGCTGACCCACAGGCGCACAGAGACAAAGCTGGTGAAGCTGGTGGTCAATGGTGTG	497
Db	1481413	GGCGGAGCGCGGTCTTCAACACGCTCAACGCGCACTCGAACGTGCGCCTTCTTCAGGAGTA	1481472
Qy	498	CGAGGGGCTCGGTTCAACACCGTGTCCGCAAGTGGACGCGGGTTCACAGCCAGCA	557
Db	1481473	CAAGTGGCGCGGCTGACCCGCAAGACATGCCGGTCGTCTCGGTGTGATTCGCCGAGGA	1481532
Qy	558	CGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAAGTGGACAGGATCTCCAA	617
Db	1481533	AGAGTCAAGTCGATCGGATCGAGTACTTGGCGGGCCAGTTGACGGCTTGGAACTACTA	1481592
Qy	618	GGCGGCGTTTCGAGTGGGCTGACCAACCCCAACCGCTGTGATCCCGACATGCAGAAGCTTGG	677
Db	1481593	CCAGACACCCCGGCGCGCGCAACCAAGTTCGTGAAGCGGTACAAGGCCAAGTACGG	1481652
Qy	678	C 678	
Db	1481653	C 1481653	

```

RESULT 10
US-10-205-032-17
; Sequence 17, Application US/10205032
; Publication No. US20030113874A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Scarfa, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
; FILE REFERENCE: 3016-2US
; CURRENT APPLICATION NUMBER: US/10/205,032
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 4725
; TYPE: DNA
; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-17

```

[illegible]

QY 244 GGTTTCAAGACCCCGGCGGGGTGTGTGTGGAGTTTCGGCAAGACCGCGACACCCACCTC 303
Db 3066393 GTCAACCGAGTCCCGCGAGGTGGGCAACGAGGGCAGCTGGCGGCAGGCACGCTG 3066334
QY 304 CTGCGGCAACCCAGGTGGCTCGGCTTCGGCGGCAAGTACAGGACCTCATCGGAAC 363
Db 3066333 CGGACGTCGACGCACTTGGCGGCACTCAGGAGTCGGTGAACGAGATGGCGGGAAC 3066274
QY 364 AAGGGTCTGGAGACCGTCAACATGGCGCGCGGCAATGACACGAGGCGCTCAACGACCTG 423
Db 3066273 CTGACCGGAGTGGCGGCATCGCGCGTGGCACCGCGGTGACCCCGCGGACCTG 3066214
QY 424 GCGAAGAAGAGGCGGCTGACCCACAGCGCGCACACAGAGCAAGCTGTGAAGCTG 483
Db 3066213 AACCTGAAGATCGACGTGAGCGCTCG-----GGCGAGATCCAGGAACCTTCAGGACTAC 3066160
QY 484 GTGGTCATGTGTGCGAGGGGTGCGGTTCAACACCGTGTCCCGCAGGTGGACGCGGG 543
Db 3066159 ATCAACAAGATGTCGCAACCTTGGCGGACACCAACCATCGCCCAAGAGAACAGGACTGG 3066100
QY 544 TTCAACAGCGACGACGCGGTGACCTTGACCGTGACGCGAGGG 585
Db 3066099 CTCAGGGCAATCTCGCCCGATCTCGCCCTGATCGAGGG 3066058

RESULT 14

US-09-846-590B-17
; Sequence 17, Application US/09846590B
; Patent No. US2002009801A1
; GENERAL INFORMATION:
; APPLICANT: Falco, S. Carl
; APPLICANT: Famodu, Layo O.
; APPLICANT: Orozco, Emil M. Jr.
; TITLE OF INVENTION: Amino Acid Decarboxylases
; FILE REFERENCE: BB-1237
; CURRENT APPLICATION NUMBER: US/09/846,590B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 60/099,493
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-846-590B-17

Query Match 6.9%; Score 51.8; DB 9; Length 1377;
Best Local Similarity 47.5%; Pred. No. 0.0002;
Matches 223; Conservative 0; Mismatches 237; Indels 9; Gaps 2;
QY 196 ACCAGCTCCATACGCTCGCCATGACATGACAACTGTACCTCGTGGGCTTCAGGAC 255
Db 700 AGGATCTCGGCGAGTCAACGACCTCAAGGATCGAGTGGCGTTCGCGCGCCTTC 759
QY 256 CCGGG---CGGGGTGTGGTGGAGTTTCGCAAGACGCGGACACCCACCTCTTCGCGCAC 312
Db 760 CCGGGGCTCAAGTCTGTGATGTGTATGCGCACCTACGCGCGCGCAAGCTGCAGGAGCAC 819
QY 313 AACCCAGTGGTTCGGCTTCGCGGCGAGTACAGGACCTATCGGCAACAGGCTGTG 372
Db 820 ATCCGGAGCGACGTTCGCTTGGCCAAAGACGTTTCGAGGACCTGTCTCGCGCGGACCGG 879
QY 373 GAGACCGTCAACATGGCGCGCGGCAAAATGACAGGCGGCTCAACGACCTGGCGGAGAG 432
Db 880 TTCAGGTGTGTGTGCGGAGAACTTCGCGCTCTGTCTTCAAGATCAGGCCGAGAAA 939
QY 433 AAGAAGCGGCTGACCCACGAGCGGACACGAGAGCAAGCTGTGAAGCTGTGTGTCATG 492
Db 940 TCGGCGCGCCCATCGCGCGCGGAGGCGGAGAGCGAGAACCGCGAGCTGATG 999
QY 493 GTGTGCGAGGGGCTGGGTTCAACACCGTGTCCCGCACGCGTGAACGCGGGGTTCAACAGC 552

Db 1000 -----GAGCGGTGAACAAGACCGGAAAGGCTTACGTGGCGCACACCGTGTGGCGGC 1053
QY 553 CAGCAGGGGTGACCTTGACCGGTGACGCGAGGGAAGCAGGTGAGAGTGGGACAGATC 612
Db 1054 AGTTCGTCTCGCTTCGCGGTGGGTCTGCTGTCAGGAGGCGGACGTCGTGCAAGC 1113
QY 613 TCCAAAGCGCGCTTCGAGTGGGTGACCAACCCACCGCTGTGATCCCG 661
Db 1114 GCGTGGAGCTCATCAAGAAGACGACCCAGATCTGTCGCCACGCG 1162

RESULT 15

US-10-205-032-15
; Sequence 15, Application US/10205032
; Publication No. US20030113874A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Yang, Xianshu
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS FOR THE BIOSYNTHESIS OF ROSARAMICIN
; FILE REFERENCE: 3016-2US
; CURRENT APPLICATION NUMBER: US/10/205,032
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 11238
; TYPE: DNA
; ORGANISM: micromonospora carbonacea subspecies aurantiaca
US-10-205-032-15

Query Match 6.8%; Score 51.2; DB 14; Length 11238;
Best Local Similarity 45.0%; Pred. No. 0.00043;
Matches 191; Conservative 0; Mismatches 233; Indels 0; Gaps 0;
QY 201 CTCATACGCTTCGCGCATACGATGACAACTGTACTCTGTGGCTTCAGGACCCCGG 260
Db 5487 CGCCATGATGTGTGTCAGCGCTCGCGACCGGAGGCGCGGCGACGAGATCTCTGC 5546
QY 261 CCGGGTGTGTGGAGTTGCGCAAGGACGCGGACACCCACCTCTCTCGGCGCAACCCGAG 320
Db 5547 CGTGTCAAGGCTCGGCCGTCAACGAGGACGCGGCGGCAACCGCCCTCACCGCCCGAA 5606
QY 321 GTGGCTCGGCTTCGCGCGCAGGTACGAGACCTCATCGGCAACAAGGCTCTGAGACCGT 380
Db 5607 CCGGCCCTCCAGGAACGCGTTCATCGGACGCGCTTGCCCGACGCGGCTTCGGCCGGA 5666
QY 381 CACCATGGGCGCGCGCAAAATGACAGGCGCGTCAACGACCTTGGCGAAGAAAGAGGC 440
Db 5667 CCAGGTGGACGCGGTGAGGCGCACCGGACCGGACCGGCGCGGCGGCGGCGGCGGCGG 5726
QY 441 GCGTACCCACAGGCGGACACGAGAGCAGTGTGAGCTGTGAGTGTGATGTCGGA 500
Db 5727 GCAGCGCTGTCTCGGCAAGTACGCGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGG 5786
QY 501 GCGGCTGCGGTTCAACACCGTGTCTCCGCAAGGTCGACGCGGCGGTTCAACAGCCAGCAG 560
Db 5787 CTCGTGAAGTCCACATCGGTCAACCCAGGCGCGCGCGGCGGCGGCGGCGGCGGCGG 5846
QY 561 GGTGACCTTGAACGTCAGCGAGGGAAGCAGGTGAGAGTGTGAGAGTGTGATCTCAAGGC 620
Db 5847 GGTGATCTTGGGCTTCGCGCACGACGCTGCGCGCACGCTGCGCGCACGCTGACGTTGGACCGGCGGCGAG 5906
QY 621 GCGC 624
Db 5907 GCGC 5910

Search completed: October 22, 2003, 08:06:27
Job time : 306 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 04:06:58 ; Search time 284 Seconds
(without alignments)
7128.798 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

Sequence: 1 atgaaagaatagtgccaaa.....ctactgcgctgctaataa 750

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	750	100.0	750	24	AA038057
2	740.8	98.8	847	18	AA079869
3	740.8	98.8	847	13	AA077761
4	740.8	98.8	978	18	AA020478
5	740.8	98.8	978	18	AA079864
6	740.8	98.8	978	18	AA077756
7	740.8	98.8	984	18	AA079863
8	740.8	98.8	985	18	AA077755

9	740.8	98.8	1161	18	AA079866	Pro-ribosome inact
10	740.8	98.8	1161	18	AA077758	RIP fusion protein
11	740.8	98.8	1422	18	AA079867	Pro-ribosome inact
12	740.8	98.8	1422	18	AA077759	RIP fusion protein
13	740.8	98.8	1683	13	AA020482	Maize RIP deriv. R
14	740.8	98.8	1683	18	AA079868	Pro-ribosome inact
15	740.8	98.8	1683	18	AA077760	RIP fusion protein
16	740.8	98.8	1695	18	AA079870	Pro-ribosome inact
17	740.8	98.8	1695	18	AA077762	RIP fusion protein
18	740.8	98.8	1722	18	AA079871	Pro-ribosome inact
19	740.8	98.8	1722	18	AA077763	RIP fusion protein
20	739.2	98.6	1422	13	AA020481	Maize RIP deriv. R
21	737.8	98.4	1029	18	AA079862	Maize single chain
22	737.8	98.4	1029	18	AA077754	RIP fusion protein
23	736.6	98.2	1161	13	AA020480	Maize RIP deriv. R
24	720.2	96.0	986	18	AA079865	Truncated pro-ribo
25	720.2	96.0	986	18	AA077757	RIP fusion protein
26	707.4	94.3	987	13	AA020479	Maize RIP deriv. R
27	707.2	94.3	987	20	AA078467	Maize KRIP derivat
28	656	87.5	909	24	AA038056	Maize pro-ribosome
29	655.8	87.4	1074	18	AA079873	Maize ribosome ina
30	654.2	87.2	1059	20	AA078470	Maize RIP-2 DNA.
31	652.8	87.0	1076	18	AA079861	Maize pro-ribosome
32	652.8	87.0	1076	18	AA077753	proRIP coding sequ
33	652.8	87.0	1105	13	AA020477	Maize proRIP sequ
34	652.8	87.0	1105	18	AA079872	Maize pro-ribosome
35	652.6	87.0	1053	20	AA078473	Maize RIP-3 DNA.
36	651.2	86.8	1076	13	AA020476	Maize proRIP. Zea
37	649.8	86.6	944	20	AA078475	Maize RIP-4 DNA.
38	649.8	86.6	1244	20	AA078479	Maize RIP-5 DNA.
39	636.8	84.9	1245	20	AA078481	Maize KRIP DNA. Z
40	510.8	68.1	1934	17	AA042302	Maize ribosomal in
41	438	58.4	444	24	AA038058	Maize ribosome ina
42	308	41.1	533	20	AA078489	Maize KRIP 3'-end
43	307.4	41.0	354	24	AA038059	Maize ribosome ina
44	113.8	15.2	240	24	AB071901	Corn tassal-derive
45	77.6	10.3	846	14	AA042301	Barley Type 1 ribo

ALIGNMENTS

RESULT 1
AA038057
ID AAD38057 standard; DNA; 750 BP.

XX AC AAD38057;

XX DT 10-SEP-2002 (first entry)

XX DE Maize processed ribosome inactivating protein (RIP-P) encoding DNA.

XX DE Maize; transgenic; transgenic plant; ribosome inactivating protein; RIP;

KW cytotoxicity; nematode resistant plant; sterility; fruit abscission;

KW viral infection; nematocide; antiviral; RIP-P DNA; ds.

XX OS Zea mays.

XX FH Key

FT misc_signal Location/Qualifiers

FT /tag= a

FT /note= "Initiation codon added by PCR primer"

FT /tag= b

FT /note= "Sequence replacing removed SacI site"

FT /tag= c

FT /note= "Stop codons added by PCR primer"

FT WO200233106-A2.

XX 25-APR-2002.

XX PD

XX RIP fusion protein

PF 15-OCT-2001; 2001WO-0B04581.
XX
PR 14-OCT-2000; 2000GB-0025225.
XX
PA (ADTE-) ADVANCED TECHNOLOGIES CAMBRIDGE LTD.
XX
PI Thomas CJR, McPherson MJ, Atkinson HJ, Neelam A;
XX
DR WPI; 2002-452339/48.
XX
XX
PT Producing transgenic plant resistant to nematode infection, comprises
PT transforming plant with chimeric gene having promoter inducible at
PT nematode feeding site, linked to sequence encoding maize ribosome
PT inactivating protein -
XX
PS Claim 7; Page 85; 89pp; English.
XX
CC The present invention relates to a novel method for producing transgenic
CC plants which harbour chimeric genes within the genome of the plant, the
CC expression of which gene causes plant cytotoxicity at a target site. The
CC method involves transforming a plant with a chimeric gene comprising a
CC promoter inducible at and/or adjacent to a target site, operably linked
CC to a coding sequence encoding a maize ribosome inactivating protein (RIP)
CC or its portion. The method is useful for producing transgenic plants
CC harbouring within the genome a chimeric gene which when expressed,
CC produces a cytotoxic protein. The target site may be a nematode feeding
CC site and by targeting the nematode feeding site, nematode resistant
CC plant can be obtained. If the target site is one or more of plant's
CC pollen, anther or tapetum, the method is useful for effecting the male
CC sterility in plants and if the target site is ovule of plant, the method
CC is directed to effecting female sterility in plants. The target site may
CC be specific parts of the flower or abscission zone of the leaf and/or
CC fruit and the method is useful for manipulating morphology of the flower
CC of a plant and to assist in or promote leaf and/or fruit abscission in
CC plants. The method is also useful for controlling viral infection. The
CC present sequence is maize processed RIP (RIP-P) DNA.
XX
SQ Sequence 750 BP; 185 A; 217 C; 232 G; 116 T; 0 other;
Query Match 100.0%; Score 750; DB 24; Length 750;
Best Local Similarity 100.0%; Pred. No. 7.1e-150;
Matches 750; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAAGAATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGCGAACTACCCCT 60
Db 1 ATGAAAGAATAGTGCACAAAGTTCACTGAATCTTCCCGTGAGGACGCGAACTACCCCT 60
QY 61 TACAGCGCCTTCATCGCGTGGTCCGGAAGAGTGTATCAAACTGACCGACCATAA 120
Db 61 TACAGCGCCTTCATCGCGTGGTCCGGAAGAGTGTATCAAACTGACCGACCATAA 120
QY 121 GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGTCCCGGAGCTATGTTCTACACA 180
Db 121 GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGTCCCGGAGCTATGTTCTACACA 180
QY 181 GAATGAAACTAGACACAGCTCCATCACTGCTCCCATATGATGACAACTGTGACCTC 240
Db 181 GAATGAAACTAGACACAGCTCCATCACTGCTCCCATATGATGACAACTGTGACCTC 240
QY 241 GTGGGCTTCAGGACCCCGGGGGGTGTGTGGAGTTCGGCAAGGACGCGACCCAC 300
Db 241 GTGGGCTTCAGGACCCCGGGGGGTGTGTGGAGTTCGGCAAGGACGCGACCCAC 300
QY 301 CTCTCGGCGACACCCAGGTGGTCTCGGCTTCGGGCGGACAGGTACAGGACCTCATCGGC 360
Db 301 CTCTCGGCGACACCCAGGTGGTCTCGGCTTCGGGCGGACAGGTACAGGACCTCATCGGC 360
QY 361 AACAGGGTCTGAGACCGTCAACATGGCGCGCGGAAATGACCGAGGCGGTCAACGAC 420
Db 361 AACAGGGTCTGAGACCGTCAACATGGCGCGCGGAAATGACCGAGGCGGTCAACGAC 420
QY 421 CTGGCGAGAGAGAGAGGGCGGTGACCCACAGCGGACACGAGAGAGCTGGTGAAG 480

Db 421 CTGGCGAGAGAGAGAGAGGGCGGTGACCCACAGGCGCGCTACCCACAGGACGAAAGCTGGTGAAG 480
QY 481 CTGGTGGTTCATGGTGTGGAGGGGCTGGGGTTCAACACCGTGTCCCGCACGGTGGACGG 540
Db 481 CTGGTGGTTCATGGTGTGGAGGGGCTGGGGTTCAACACCGTGTCCCGCACGGTGGACGG 540
QY 541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGAGAAG 600
Db 541 GGGTTCAACAGCAGCAGCGGGGTGACCTTGACCGTGAACGAGGGAAGCAGGTGAGAAG 600
QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC 660
Db 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC 660
QY 661 GACATGCGAAGCTTTGGCATCAAGGATGAAGAACGAGCAGGAGGATCGTTGGCTCGTT 720
Db 661 GACATGCGAAGCTTTGGCATCAAGGATGAAGAACGAGCAGGAGGATCGTTGGCTCGTT 720
QY 721 AAGAATCAAACTACTGCGCTGCCTAATAA 750
Db 721 AAGAATCAAACTACTGCGCTGCCTAATAA 750
RESULT 2
AAT79869
ID AAT79869 standard; DNA; 847 BP.
XX
AC AAT79869;
XX
DT 25-MAR-2003 (updated)
DT 01-DEC-1997 (first entry)
XX
DE Pro-ribosome inactivating protein gene clone RDT-BHSR.
XX
KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
KW internal linker; Barley Translation Inhibitor; Trichosanthin;
KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
KW post-translational modification; cancer; neoplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immune deficiency syndrome; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
CDS 51..845
FT /*tag= a
FT /note= "no stop codon given"
XX
PN US5646026-A.
XX
PD 08-JUL-1997.
XX
PF 07-JUN-1995; 95US-0485286.
XX
PR 09-DEC-1992; 92US-0987927.
PR 11-JUN-1990; 90US-0535636.
PR 26-JAN-1995; 95US-0378761.
PR 07-JUN-1995; 95US-0485286.
XX
PA (DOWC) DOWELANCO.
XX
XX Hey TD, Morgan AER, Walsh TA;
PI WPI; 1997-362934/33.
DR P-PSDB; AAN25131.
XX
PT DNA encoding pro-ribosome inactivating proteins - inactive
PT precursors of ribosome inactivating proteins; can be expressed in
PT eukaryotic cells without causing cell death
XX
PS Claim 2; Column 73-76; 186pp; English.
XX

CC AAT79869 encodes a single chain maize pro-ribosome inactivating protein (proRIP). The sequence was engineered to allow the introduction of a synthetic linker separating the alpha and beta units of the RIP protein to form an inactive form of RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different Panacoidae RIPs may be produced with an internal linker including: Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin, Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the proRIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins. CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 847 BP; 212 A; 240 C; 254 G; 141 T; 0 other;
 SQ

Query Match 98.8%; Score 740.8; DB 18; Length 847;
 Best Local Similarity 99.7%; Pred. No. 6.5e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGGCAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 60
 DB |||||
 QY 51 ATGAAAGAAATAGTGGCAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 110
 DB |||||
 QY 61 TACAGCGCCTTATCGCGTCCGTCGGGAAAGACGTGATCAAACTGCACCCGACATAA 120
 DB |||||
 QY 111 TACAGCGCCTTATCGCGTCCGTCGGGAAAGACGTGATCAAACTGCACCCGACATAA 170
 DB |||||
 QY 121 GGGATCTTCAGCCCGTGTCCACCGGAGAAAGTCCCGAGCTATGGTTCTACACA 180
 DB |||||
 QY 171 GGGATCTTCAGCCCGTGTCCACCGGAGAAAGTCCCGAGCTATGGTTCTACACA 230
 DB |||||
 QY 181 GAACTGAAAACTAGGACCACTCCATCACGCTCGCCATCGCATGACACCTGTACCTC 240
 DB |||||
 QY 231 GAGCTCAAACTAGGACCACTCCATCACGCTCGCCATCGCATGACACCTGTACCTC 290
 DB |||||
 QY 241 GTGGGCTTCAGGACCCCGCGGGGTGTGGTGGAGTTGGCAAGGACGCGCACCCAC 300
 DB |||||
 QY 291 GTGGGCTTCAGGACCCCGCGGGGTGTGGTGGAGTTGGCAAGGACGCGCACCCAC 350
 DB |||||
 QY 301 CTCCTCGGCGACAAACCCAGGTGGTCCGTCGGCGGAGGTACAGACCTCATCGGC 360
 DB |||||
 QY 351 CTCCTCGGCGACAAACCCAGGTGGTCCGTCGGCGGAGGTACAGACCTCATCGGC 410
 DB |||||
 QY 361 AACAGGGTCTGAGACCGCTCACTATGGCGCGCGGAAATGACAGGGCGCTCAACGAC 420
 DB |||||
 QY 411 AACAGGGTCTGAGACCGCTCACTATGGCGCGCGGAAATGACAGGGCGCTCAACGAC 470
 DB |||||
 QY 421 CTGGCGAAGAAAGAGCGGTGTACCCACAGCGCGACACGAAAGACGAAGTGTGTAAG 480
 DB |||||
 QY 471 CTGGCGAAGAAAGAGCGGTGTACCCACAGCGCGACACGAAAGACGAAGTGTGTAAG 530
 DB |||||
 QY 481 CTGGTGTCTATGTGTGCGAGGGGCTCGGTTCAACACCGTGTCCGACGCTGGAGCG 540
 DB |||||
 QY 531 CTGGTGTCTATGTGTGCGAGGGGCTCGGTTCAACACCGTGTCCGACGCTGGAGCGG 590
 DB |||||
 QY 541 GGGTTCAACAGCCAGCACCGGGGTGACCTTGACCGTGACGAGGGGAGAGGTGCAGAG 600
 DB |||||
 QY 591 GGGTTCAACAGCCAGCACCGGGGTGACCTTGACCGTGACGAGGGGAGAGGTGCAGAG 650
 DB |||||
 QY 601 TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660
 DB |||||
 QY 651 TGGGACAGGATCTCCAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
 DB |||||
 QY 661 GACATCGAGAGCTTGGCATCAGGATAGAAAGAGACGAGGATCGTTGGCGTCGTT 720
 DB |||||

Db 711 GACATGCAGAGCTTGGCATCAAGGATAAGAACAGCAGCAGGATCGTTGGCTCGTT 770
 QY 721 AGAATCAAACTACTGCCGCTGCC 744
 Db 771 AGAATCAAACTACTGCCGCTGCC 794

RESULT 3
 AAT77761
 ID AAT77761 standard; DNA; 847 BP.
 XX
 AC AAT77761;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 DE RIP fusion protein, RDT-BHSR coding sequence.
 XX
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivator; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 CDS 51..845
 FT /*tag= a
 FT /product= RDT-BHSR
 XX
 PN US535384-A.
 XX
 XX 03-JUN-1997.
 XX
 XX 26-JAN-1995; 95US-0378761.
 XX
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 XX (DOWC) DOWELANCO.
 XX
 PI Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-309831/28.
 DR P-PSDB; AAM21718.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 PS Claim 4; Column 73-76; 121pp; English.
 XX
 CC The sequences given in AAT77754-63 encode fusion proteins which are
 CC examples of Ribosome Inactivating Proteins. RIPs are potent inhibitors
 CC of eukaryotic protein synthesis. They possess a highly specific
 CC N-glycosidase activity which cleaves the glycosidic bond of adenine
 CC 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected
 CC T cells. The inactive proRIP proteins make it possible to provide
 CC protein synthesis inhibitors with uses in practical and improved
 CC ways not before possible. The RIP can be used to make cytotoxic
 CC conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 847 BP; 212 A; 240 C; 254 G; 141 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 847;
 Best Local Similarity 99.7%; Pred. No. 6.5e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTGGCAAGTTCACTGAATCTTCCCGTGAGAGCGGAACACTACCT 60
 |||||

Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 110
Qy 61 TACAGCGCTTCATCGCGTCCGTCGCGAAGACGTGATCAAAACACTGACACCATATAA 120
Db 111 TACAGCGCTTCATCGCGTCCGTCGCGAAGACGTGATCAAAACACTGACACCATATAA 170
Qy 121 GGGATCTTCCAGCCCGTGTGTCACCGGAGAAAGGTCCTCCGAGCTATGTTTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGTCACCGGAGAAAGGTCCTCCGAGCTATGTTTACACA 230
Qy 181 GAACTGAAACTAGAACCGAGTCCATCAGCTCGCCATACGATGACGACCTGACCTC 240
Db 231 GAGCTCAAACTAGAACCGAGTCCATCAGCTCGCCATACGATGACGACCTGACCTC 290
Qy 241 GTGGGCTTCAGACCCCGCGGGGTGTGTTGGAGTTCCGCAAGACCGGACACCCAC 300
Db 291 GTGGGCTTCAGACCCCGCGGGGTGTGTTGGAGTTCCGCAAGACCGGACACCCAC 350
Qy 301 CTCCTCGGCGACAAACCCAGTGGCTTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGTGGCTTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 410
Qy 361 AACAGGCTTCGAGACCGTCACTATGGCGCGCGCGAAATGACACGAGCGCTCAACGAC 420
Db 411 AACAGGCTTCGAGACCGTCACTATGGCGCGCGCGAAATGACACGAGCGCTCAACGAC 470
Qy 421 CTGGCGAAGAAAGAGCGGCTGACCCACGAGCGGCTGACCGGAGGAGGAGTGGTGAAG 480
Db 471 CTGGCGAAGAAAGAGCGGCTGACCCACGAGCGGCTGACCCACGAGCGGAGGAGTGGTGAAG 530
Qy 481 CTGGTGGTTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGACGCTGCGG 540
Db 531 CTGGTGGTTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGACGCTGCGG 590
Qy 541 GGGTTCAACAGCCAGACCGGGGTGACTTGAACCGTACGCGGAGGAGGAGTGGTGAAG 600
Db 591 GGGTTCAACAGCCAGACCGGGGTGACTTGAACCGTACGCGGAGGAGGAGTGGTGAAG 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCCCGTGTGATCCCG 660
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCCCGTGTGATCCCG 710
Qy 661 GACATGACAGAGCTTGGCTCAAGGATAGAAAGACGAGGAGGATGCTGCTCGTT 720
Db 711 GACATGACAGAGCTTGGCTCAAGGATAGAAAGACGAGGAGGATGCTGCTCGTT 770
Qy 721 AGAATCAAACTACTGCGCGTGC 744
Db 771 AGAATCAAACTACTGCGCGTGC 794

RESULT 4

AAQ20478
ID AAQ20478 standard; DNA; 978 BP.
XX
AC AAQ20478;
XX
DT 13-APR-1992 (first entry)
XX
DE Maize RIP deriv. RDT.
XX
KW Ribosome-inactivating protein; alpha RIP; beta RIP; alpha-beta RIP;
KW HIV; tumour; ss.
XX
OS Zea mays.
XX
PH Key Location/Qualifiers
CDS 51..815
FT /*tag= a
FT /label= RDT
FT /note= "RIP deriv."
XX
PN BP46222-A.

XX 15-JAN-1992.
PD
XX
XX 10-JUN-1991; 91EP-0201436.
PF
XX
XX 11-JUN-1990; 90US-0535636.
PR
XX
XX (DOWC) DOWELANCO.
PA
PI Walsh TA, Hey TD, Morgan AER;
XX
XX WPI; 1992-017847/03.
DR P-PSDB; AAR20081.
XX
XX New plant ribosome inactivating proteins and inactive precursors
PT - expressed in eukaryotic cells, useful e.g. in tumour or HIV
PT treatment, and new DNA encoding them
PT
XX Disclosure; Page 25; 40pp; English.
XX
XX The RIP deriv., RDT, encodes a protein (28.233 kD) with a truncated
CC leader, deleted linker and truncated carboxy terminus. It appears
CC to be a more potent inhibitor of protein synthesis than R30-DL
CC (having the linker and leader fragments deleted from proRIP).
CC See also AAQ20476-82.
XX
XX Sequence 978 BP; 250 A; 271 C; 274 G; 183 T; 0 other;
SQ
Query Match 98.8%; Score 740.8; DB 13; Length 978;
Best Local Similarity 99.7%; Pred. No. 6.6e-148; Indels 0; Gaps 0;
Matches 742; Conservative 0; Mismatches 2;
Qy 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCTT 110
Qy 61 TACAGCGCTTCATCGCGTCCGTCGCGAAGACGTGATCAAAACACTGACACCATATAA 120
Db 111 TACAGCGCTTCATCGCGTCCGTCGCGAAGACGTGATCAAAACACTGACACCATATAA 170
Qy 121 GGGATCTTCCAGCCCGTGTGTCACCGGAGAAAGGTCCTCCGAGCTATGTTTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGTCACCGGAGAAAGGTCCTCCGAGCTATGTTTACACA 230
Qy 181 GAACTGAAACTAGGACACCGTCCATCAGCTCGCCATACGATGACACCACTGTACCTC 240
Db 231 GAGCTCAAACTAGGACACCGTCCATCAGCTCGCCATACGATGACACCACTGTACCTC 290
Qy 241 GTGGGCTTCAGACCCCGCGGGGTGTGTTGGAGTTCCGCAAGACCGGACACCCAC 300
Db 291 GTGGGCTTCAGACCCCGCGGGGTGTGTTGGAGTTCCGCAAGACCGGACACCCAC 350
Qy 301 CTCCTCGGCGACAAACCCAGTGGCTTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGTGGCTTCGGCTTCGGCGGAGGTACACGACCTCATCGGC 410
Qy 361 AACAGGCTTCGAGACCGTCACTATGGCGCGCGCGAAATGACACGAGCGCTCAACGAC 420
Db 411 AACAGGCTTCGAGACCGTCACTATGGCGCGCGCGCGAAATGACACGAGCGCTCAACGAC 470
Qy 421 CTGGCGAAGAAAGAGCGGCTGACCCACGAGCGGCTGACCGGAGGAGGAGTGGTGAAG 480
Db 471 CTGGCGAAGAAAGAGCGGCTGACCCACGAGCGGCTGACCCACGAGCGGAGGAGTGGTGAAG 530
Qy 481 CTGGTGGTTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGACGCTGCGG 540
Db 531 CTGGTGGTTCATGGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCCGACGCTGCGG 590
Qy 541 GGGTTCAACAGCCAGACCGGGGTGACTTGAACCGTACGCGGAGGAGGAGTGGTGAAG 600
Db 591 GGGTTCAACAGCCAGACCGGGGTGACTTGAACCGTACGCGGAGGAGGAGTGGTGAAG 650
Qy 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCCACCGCCCGTGTGATCCCG 660

Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGCTGACACCCACCGCTGTGATCCCC 710
QY 661 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 720
Db 711 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 770
QY 721 AAGAATCAAACTACTCCCGTGCC 744
Db 771 AAGAATCAAACTACTCCCGTGCC 794
RESULT 5
AAT79864
ID AAT79864 standard; DNA; 978 BP.
XX
AC AAT79864;
XX
DT 25-MAR-2003 (updated)
DT 01-DEC-1997 (first entry)
XX
XX Truncated pro-ribosome inactivating protein gene clone RDT.
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
XX internal linker; Barley Translation Inhibitor; Trichosanthin;
XX Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
XX Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
XX post-translational modification; cancer; neoplasia; HIV; AIDS;
XX human immunodeficiency virus; acquired immune deficiency syndrome; ss.
XX
OS Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 51..815
XX /*tag= a
XX
XX US5646026-A.
XX
XX 08-JUL-1997.
XX
XX 07-JUN-1995; 95US-0485286.
XX
XX 09-DEC-1992; 92US-0987927.
XX 11-JUN-1990; 90US-0535636.
XX 26-JAN-1995; 95US-0378761.
XX 07-JUN-1995; 95US-0485286.
XX
XX (DOWC) DOWELANCO.
XX
XX Hey TD, Morgan AER, Walsh TA;
XX
XX WPI: 1997-362934/33.
XX P-PSDB; AAW25126.
XX
XX DNA encoding pro-ribosome inactivating proteins - inactive
XX precursors of ribosome inactivating proteins; can be expressed in
XX eukaryotic cells without causing cell death
XX
XX Claim 2; Column 51-52; 186pp; English.
XX
XX AAT79864 encodes a single chain maize pro-ribosome inactivating protein
XX (proRIP) having a truncated leader sequence and carboxy terminus
XX engineered for expression in Escherichia coli.
XX The sequence contains no linker separating the alpha and beta subunit
XX regions and was shown to be a potent inhibitor of protein synthesis.
XX proRIP sequences can be engineered to contain a selectively removable
XX internal peptide linker sequence separating the alpha and beta units
XX of the RIP protein to form an inactive form of RIP. When separated
XX the two units regain activity and are capable of inactivating eukaryotic
XX ribosomes and hence preventing protein production. Many different
XX Panacoidae RIPs may be produced with an internal linker including:
XX Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A

CC A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin,
CC Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in
CC the construction of therapeutic toxins targeted to specific cells such
CC as tumour cells via the attachment of a targeting polypeptide, e.g. a
CC monoclonal antibody. A further use is in HIV therapy (see US4869903).
CC There is interest in expressing RIP recombinantly in host eukaryotic
CC cells, because of the capacity to provide correct post-translational
CC processing. However, RIPs effectively inhibit protein synthesis in
CC eukaryotic cells resulting in cell death. Since the proRIP proteins
CC are not cytotoxic to eukaryotic cells, they can be recombinantly
CC expressed in such cells and then converted to active RIP proteins.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
XX
XX Sequence 978 BP; 250 A; 271 C; 275 G; 182 T; 0 other;
QY Query Match 98.8%; Score 740.8; DB 18; Length 978;
Best Local Similarity 99.7%; Pred. No. 6.6e-148; Indels 0; Gaps 0;
Matches 742; Conservative 0; Mismatches 2;
Db 1 ATGAAAAGAAATAGTGCCTAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 60
51 ATGAAAAGAAATAGTGCCTAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAATACCT 110
QY 61 TACAGCGCTTCATCGCTGCTCGGAAAGACGTATCAAAACACTGCACCCACCAATAA 120
Db 111 TACAGCGCTTCATCGCTGCTCGGAAAGACGTATCAAAACACTGCACCCACCAATAA 170
QY 121 GGGATCTTCCAGCCCGTGTGCTGCACCGGAGAGAGGTCCCGAGGTATGTTTACACA 180
Db 171 GGGATCTTCCAGCCCGTGTGCTGCACCGGAGAGAGGTCCCGAGGTATGTTTACACA 230
QY 181 GAACTGAAATAGGACCAAGTCCATCAGCTCGCCATACGATGACAACTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCAAGTCCATCAGCTCGCCATACGATGACAACTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGCGGGTGTGTTGGAGTTTGGCAAGGACGCGACACCCAC 300
Db 291 GTGGGCTTCAGGACCCCGGCGGGTGTGTTGGAGTTTGGCAAGGACGCGACACCCAC 350
QY 301 CTCCTCGGCGACAAACCCAGGTGGTTCGGCTTCGGCGGAGGTACCCAGACCTCATCGGC 360
Db 351 CTCCTCGGCGACAAACCCAGGTGGTTCGGCTTCGGCGGAGGTACCCAGACCTCATCGGC 410
QY 361 AACAAAGGTCTCGAGACCGTCCATATGGCCCGCGCGAATGACAGGCGCGTCAACGAC 420
Db 411 AACAAAGGTCTCGAGACCGTCCATATGGCCCGCGCGAATGACAGGCGCGTCAACGAC 470
QY 421 CTGGCGAAGAAAGAGGCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGGTGAAG 480
Db 471 CTGGCGAAGAAAGAGGCGGCTGACCCACAGGCGGACACGAGAGCAAGCTGGTGAAG 530
QY 481 CTGGTGGTTCATGTTGTCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGG 540
Db 531 CTGGTGGTTCATGTTGTCGAGGGGCTGCGGTTCAACACCGTGTCCCGCACGGTGGACGG 590
QY 541 GGGTTCAACAGCCAGCACCGGGTGAACCTTGAACCGTGAACAGCGGGAAGCAGGTGCAAGAG 600
Db 591 GGGTTCAACAGCCAGCACCGGGTGAACCTTGAACCGTGAACAGCGGGAAGCAGGTGCAAGAG 650
QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGCTGACACCCACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGCTGACACCCACCGCTGTGATCCCC 710
QY 661 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 720
Db 711 GACATGCAAGCTTGGCATCAAGGATAGAGACGAGGATCGTTCGGCTCGTT 770
QY 721 AAGAATCAAACTACTCCCGTGCC 744
Db 771 AAGAATCAAACTACTCCCGTGCC 794
RESULT 6

ID	Accession	Standard	DNA	Length	Score	Pred.	Mismatches	Indels	Gaps
AA77756	AA77756	standard	DNA; 978 BP.	978	98.8%	99.7%	0	0	0
XX	AC	AA77756;							
DT	25-MAR-2003	(updated)							
DT	26-SEP-1997	(first entry)							
DE	RIP fusion protein, RDT coding sequence.								
XX	pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;								
KW	inactivation; eukaryotic ribosome; alpha fragment; beta fragment;								
KW	inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;								
KW	rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.								
XX	Synthetic.								
OS	Key	Location/Qualifiers							
XX	CDS	51..815							
FT	/tag= a								
FT	/product= RDT								
US5635384-A.									
PN	03-JUN-1997.								
XX	26-JAN-1995;	95US-0378761.							
XX	09-DEC-1992;	92US-0987927.							
PR	11-JUN-1990;	90US-053636.							
PR	26-JAN-1995;	95US-0378761.							
XX	(DOWC) DOWELANCO.								
PA	Hey TD, Morgan AER, Walsh TA;								
PI	WPI; 1997-309831/28.								
DR	P-PSDB; AA21713.								
XX	Inactive precursor of maize ribosome-inactivating protein - also								
PT	chimeric ribosome-inactivating protein precursors containing								
PT	internal linker sequences								
XX	Claim 4; Column 49-52; 121pp; English.								
XX	The sequences given in AA77754-63 encode fusion proteins which are								
CC	examples of Ribosome Inactivating Proteins. RIPS are potent inhibitors								
CC	N-glycosylase activity which cleaves the glycosidic bond of adenine								
CC	4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit								
CC	cellular proliferation of cells, e.g. cancer cells and HIV-infected								
CC	T cells. The inactive proRIP proteins make it possible to provide								
CC	protein synthesis inhibitors with uses in practical and improved								
CC	ways not before possible. The RIP can be used to make cytotoxic								
CC	conjugates.								
CC	(Updated on 25-MAR-2003 to correct PF field.)								
XX	Sequence 978 BP; 250 A; 271 C; 275 G; 182 T; 0 other;								
SQ	Query Match	98.8%; Score 740.8; DB 18; Length 978;							
Db	Best Local Similarity	99.7%; Pred. No. 6.6e-148;							
Yy	Matches 742; Conservative	0; Mismatches 2; Indels 0; Gaps 0;							
Qy	1 ATGAAAGATAGTGCCTCAAGTTACTGTAAATCTTCCTCGGGAGGACGCCAATACCT	60							
Db	51 ATGAAAGATAGTGCCTCAAGTTACTGTAAATCTTCCTCGGGAGGACGCCAATACCT	110							
Qy	61 TAGAGCGCTTCATCGCTCGGTTCGGAAGAAGTGATCAACAACCTGACCGCATATAA	120							
Db	111 TAGAGCGCTTCATCGCTCGGTTCGGAAGAAGTGATCAACAACCTGACCGCATATAA	170							
Qy	121 GGGATCTTCAGCCCGTGTGCCACCGGAGAAAGAGTCCCGGAGCTATGGTTCTACACA	180							

XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX (DOWC) DOWELANCO.
 XX Hey TD, Morgan AER, Walsh TA;
 XX WPI; 1997-362934/33.
 DR P-PSDB; AAW21125.
 XX
 PT DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 PS Claim 2; Column 47-50; 186pp; English.
 XX
 CC AAT79863 encodes a single chain maize pro-ribosome inactivating protein
 CC (proRIP) with no leader sequence and no linker separating the alpha
 CC and beta units. proRIP sequences can be engineered to contain a
 CC selectively removable internal peptide linker sequence separating the
 CC alpha and beta units of the RIP protein to form an inactive form of RIP.
 CC When separated the two units regain activity and are capable of
 CC inactivating eukaryotic ribosomes and hence preventing protein
 CC production. Many different Panicoideae RIPs may be produced with an
 CC internal linker including: Barley Translation Inhibitor, Trichosanthin,
 CC Ricin A-chain, Abrin-A A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus
 CC communis agglutinin, Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs
 CC can be used in the construction of therapeutic toxins targeted to
 CC specific cells such as tumour cells via the attachment of a targeting
 CC polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
 CC (see US4869903). There is interest in expressing RIP recombinantly in
 CC host eukaryotic cells, because of the capacity to provide correct
 CC post-translational processing. However, RIPs effectively inhibit protein
 CC synthesis in eukaryotic cells resulting in cell death. Since the proRIP
 CC proteins are not cytotoxic to eukaryotic cells, they can be
 CC recombinantly expressed in such cells and then converted to active RIP
 CC proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 984 BP; 255 A; 270 C; 279 G; 180 T; 0 other;
 Query Match 98.8%; Score 740.8; DB 18; Length 984;
 Best Local Similarity 99.7%; Pred. No. 6.6e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAGAATAGTGCCTAAAGTTTCACTGAAATCTTCCCGTGGAGACGGAACCTACCTT 60
 DB |||||
 QY 37 ATGAAAGAATAGTGCCTAAAGTTTCACTGAAATCTTCCCGTGGAGACGGAACCTACCTT 96
 DB |||||
 QY 61 TACAGCGCTTTCATCCGTCGGTCCGGAAGAGCTGATCAAAACACATGCACCGACCATATAA 120
 DB |||||
 QY 97 TACAGCGCTTTCATCCGTCGGTCCGGAAGAGCTGATCAAAACATGCACCGACCATATAA 156
 DB |||||
 QY 121 GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGGTCCCGGAGCTATGGTTCTACACA 180
 DB |||||
 QY 157 GGGATCTTCCAGCCCGTGTGTCACCGGAGAGAGGTCCCGGAGCTATGGTTCTACACA 216
 DB |||||
 QY 181 GAACTGAAACTAGGACCGAGTCCATCAGCTGCCATACGATCGATGACAACTGTACCTC 240
 DB |||||
 QY 217 GAGCTCAAAACTAGGACCGAGTCCATCAGCTGCCATACGATCGATGACAACTGTACCTC 276
 DB |||||
 QY 241 GTGGGTTTCAGGACCCCGGGCGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 300
 DB |||||
 QY 277 GTGGGTTTCAGGACCCCGGGCGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 336
 DB |||||
 QY 301 CTCCTCGGCGACAACCCCGAGTGGCTCGGCTTCGGGGCGGAGGTACAGGACCTCATCGGC 360
 DB |||||
 QY 337 CTCCTCGGCGACAACCCCGAGTGGCTCGGCTTCGGGGCGGAGGTACAGGACCTCATCGGC 396
 DB |||||
 QY 361 AACAGGGTCTGAGACCGGTCAACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGAC 420

DB |||||
 QY 397 AACAGGGTCTGAGACCGGTCAACCATGGGCGCGGAAATGACACGAGGCGCGTCAACGAC 456
 DB |||||
 QY 421 CTGGCGAGAGAAAGAGCGGCTACCCACAGGCGCGACACCAAGAGCGAGCTGGTGAAG 480
 DB |||||
 QY 457 CTGGCGAGAGAAAGAGCGGCTACCCACAGGCGCGACACCAAGAGCGAGCTGGTGAAG 516
 DB |||||
 QY 481 CTGGTGGTTCATGGTGTGCGAGGGGTGCGGTTTCAACACCGTGTCCCGCACGCTGGACGCG 540
 DB |||||
 QY 517 CTGGTGGTTCATGGTGTGCGAGGGGTGCGGTTTCAACACCGTGTCCCGCACGCTGGACGCG 576
 QY 541 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGGTGACGCGAGGGAAGCAGGTGCAGAA 600
 DB |||||
 QY 577 GGGTTCAACAGCCAGCAGCGGGGTGACCTTGACCGGTGACGCGAGGGAAGCAGGTGCAGAA 636
 QY 601 TGGGACAGGATCTCCAAGGCGGCTTCGAGTGGGTGACCGACCCACCGCTGTGATCCCG 660
 DB |||||
 QY 637 TGGGACAGGATCTCCAAGGCGGCTTCGAGTGGGTGACCGACCCACCGCTGTGATCCCG 696
 QY 661 GACATGCAGAACTTGGCATCAAGGATAAGAACGAGCAGCGAGGATCGTTGCGCTCGTT 720
 DB |||||
 QY 697 GACATGCAGAACTTGGCATCAAGGATAAGAACGAGCAGCGAGGATCGTTGCGCTCGTT 756
 QY 721 AAGAATCAAACTACTGCGCGCTGCC 744
 DB |||||
 QY 757 AAGAATCAAACTACTGCGCGCTGCC 780
 DB |||||
 RESULT 8
 AAT77755
 ID AAT77755 standard; DNA; 985 BP.
 XX
 AC AAT77755;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 DE
 DE RIP fusion protein, R30-DL coding sequence.
 XX
 KW pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 37..822
 FT /*tag= a
 FT /product= R30-DL
 XX
 XX US5635384-A.
 PD 03-JUN-1997.
 XX
 PF 26-JAN-1995; 95US-0378761.
 XX
 PR 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 PA (DOWC) DOWELANCO.
 XX
 PI Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-309831/28.
 DR P-PSDB; AAW211712.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 PS Claim 4; Column 45-48; 121pp; English.

CC The sequences given in AAT7754-63 encode fusion proteins which are
CC examples of Ribosome Inactivating Proteins. RIPS are potent inhibitors
CC of eukaryotic protein synthesis. They possess a highly specific
CC N-glycosidase activity which cleaves the glycosidic bond of adenine
CC 4324 of rat liver ribosomal 28S RNA. RIPs selectively inhibit
CC cellular proliferation of cells, e.g. cancer cells and HIV-infected
CC T cells. The inactive proRIP proteins make it possible to provide
CC protein synthesis inhibitors with uses in practical and improved
CC ways not before possible. The RIP can be used to make cytotoxic
CC conjugates.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 985 BP; 255 A; 271 C; 279 G; 180 T; 0 other;
Query Match 98.8%; Score 740.8; DB 18; Length 985;
Best Local Similarity 99.7%; Pred. No. 6.6e-148;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGGAACTACCCCT 60
Db |||||
QY 37 ATGAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGGACGGAACTACCCCT 96
Db |||||
QY 61 TAGAGCGCTTCATCGGTCGGTCCGGAAGAGATGATCAACACTGACCGACCATATAA 120
Db |||||
QY 97 TAGAGCGCTTCATCGGTCGGTCCGGAAGAGATGATCAACACTGACCGACCATATAA 156
Db |||||
QY 121 GGGATCTTCCAGCCCGTGTGTCACACCGAGAGAGTCCCGAGCTATGTTCTACACA 180
Db |||||
QY 157 GGGATCTTCCAGCCCGTGTGTCACACCGAGAGAGTCCCGAGCTATGTTCTACACA 216
Db |||||
QY 181 GAGTGAATACTAGGACAGCTCATCACTGCGCCATACGATGGAACACCTGTACCTC 240
Db |||||
QY 217 GAGCTCAAAACTAGGACAGCTCATCACTGCGCCATACGATGGAACACCTGTACCTC 276
Db |||||
QY 241 GTGGCTTTCAGGACCCCGGGGGTGTGTGGAGTGTGGCAAGGACGGACACCCAC 300
Db |||||
QY 277 GTGGCTTTCAGGACCCCGGGGGTGTGTGGAGTGTGGCAAGGACGGACACCCAC 336
Db |||||
QY 301 CTCCTCGGCGACACCCCGAGTGGCTCGGCTTCCGCGGAGGTACAGGACCTCATCGGC 360
Db |||||
QY 337 CTCCTCGGCGACACCCCGAGTGGCTCGGCTTCCGCGGAGGTACAGGACCTCATCGGC 396
Db |||||
QY 361 AACAGGCTTGGAGACCGTCAACATGGCGCGGCCGGAATGACAGGCGCGTCAACGAC 420
Db |||||
QY 397 AACAGGCTTGGAGACCGTCAACATGGCGCGGCCGGAATGACAGGCGCGTCAACGAC 456
Db |||||
QY 421 CTGCGGAAGAGAGAGAGCGGCTGACCCACAGCGCGACAGAGAGAGCTGTGAAG 480
Db |||||
QY 457 CTGCGGAAGAGAGAGAGCGGCTGACCCACAGCGCGACAGAGAGAGCTGTGAAG 516
Db |||||
QY 481 CTGCTGTCTATGTGTCCGAGGGGCTCGGCTTCAACACCGCTGCCCGAGCGGAGCGG 540
Db |||||
QY 517 CTGCTGTCTATGTGTCCGAGGGGCTCGGCTTCAACACCGCTGCCCGAGCGGAGCGG 576
Db |||||
QY 541 GGGTTCAACGACGACGCGGGGTGACCTTGAACCTGACGAGGGGAAGAGGTCGAGAAG 600
Db |||||
QY 577 GGGTTCAACGACGACGCGGGGTGACCTTGAACCTGACGAGGGGAAGAGGTCGAGAAG 636
Db |||||
QY 601 TGGGACAGGATCTCCAGGCGGCTTCAGTGGCTGACACCCACCGCTGTGATCCCC 660
Db |||||
QY 637 TGGGACAGGATCTCCAGGCGGCTTCAGTGGCTGACACCCACCGCTGTGATCCCC 696
Db |||||
QY 661 GACATGACAGAGCTTGGCATCAAGGATAAGAAAGACGAGGATCGTTGGCGTGGTT 720
Db |||||
QY 697 GACATGACAGAGCTTGGCATCAAGGATAAGAAAGACGAGGATCGTTGGCGTGGTT 756
Db |||||
QY 721 AAGATCAAACTACTGCGGTGCC 744
Db |||||
QY 757 AAGATCAAACTACTGCGGTGCC 780
Db |||||

RESULT 9

AAT79866
ID AAT79866 standard; DNA; 1161 BP.
XX AC AAT79866;
XX AC AAT79866;
DT 25-MAR-2003 (updated)
DT 01-DEC-1997 (first entry)
XX DE Pro-ribosome inactivating protein gene clone RDT-A.
XX XX
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
XX internal linker; Barley Translation Inhibitor; Trichosanthin;
XX Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
XX Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
XX therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
XX post-translational modification; cancer; neoplasia; HIV; AIDS;
XX human immunodeficiency virus; acquired immune deficiency syndrome; ss.
XX Zea mays.
XX XX
XX Key Location/Qualifiers
XX CDS 51..938
XX /*tag= a
XX US5646026-A.
XX 08-JUL-1997.
XX 07-JUN-1995; 95US-0485286.
XX 09-DEC-1992; 92US-0987927.
XX 11-JUN-1990; 90US-0535636.
XX 26-JAN-1995; 95US-0378761.
XX 07-JUN-1995; 95US-0485286.
XX (DOWC) DOWELANCO.
XX Hey TD, Morgan ABR, Walsh TA;
XX WPI; 1997-362934/33.
XX P-PSDB; AAW25128.
XX DNA encoding pro-ribosome inactivating proteins - inactive
XX precursors of ribosome inactivating proteins; can be expressed in
XX eukaryotic cells without causing cell death
XX Claim 2; Column 57-60; 186pp; English.
XX AAT79866 encodes a single chain maize pro-ribosome inactivating protein
XX (proRIP) having a truncated leader sequence and carboxy terminus
XX engineered for expression in Escherichia coli and which binds to
XX immunoglobulin IgG. The construct has a sequence encoding the single
XX antibody binding region (ABR) domain from Staphylococcus aureus antibody
XX binding protein A (ABR-A) inserted into a BamHI site. The sequence
XX contains no linker separating the alpha and beta subunit regions and
XX was shown to be a potent inhibitor of protein synthesis and bound
XX specifically to IgG.
XX proRIP sequences can be engineered to contain a selectively removable
XX internal peptide linker sequence separating the alpha and beta units
XX of the RIP protein to form an inactive form of RIP. When separated
XX the two units regain activity and are capable of inactivating eukaryotic
XX ribosomes and hence preventing protein production. Many different
XX Panacoidae RIPS may be produced with an internal linker including:
XX Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A
XX A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin,
XX Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPS can be used in
XX the construction of therapeutic toxins targeted to specific cells such
XX as tumour cells via the attachment of a HIV therapy (see US4869903).
XX There is interest in expressing RIP recombinantly in host eukaryotic
XX cells, because of the capacity to provide correct post-translational
XX processing. However, RIPS effectively inhibit protein synthesis in
XX eukaryotic cells resulting in cell death. Since the proRIP proteins

QY 301 CTCCTCGGCGACACCCAGTGGCTTGGCTTGGCGGCGAGTACCGAGACCTCATCGGC 360
 Db |
 QY 351 CTCCTCGGCGACACCCAGTGGCTTGGCTTGGCGGCGAGTACCGAGACCTCATCGGC 410
 Db |
 QY 361 AACAGGGTCTGGAGACCGTCAACATGGCGCGCCGAAATGACACAGGCGCTCAACGAC 420
 Db |
 QY 411 AACAGGGTCTGGAGACCGTCAACATGGCGCGCCGAAATGACACAGGCGCTCAACGAC 470
 QY 421 CTGCGGAAGAGAAAGAGGGCGGTGACCCACAGCGCCGACACGAAAGACAGCTCGTGAAG 480
 Db |
 QY 471 CTGCGGAAGAGAAAGAGGGCGGTGACCCACAGCGCCGACACGAAAGACAGCTCGTGAAG 530
 QY 481 CTGCTGTCTGTGTGTGCGAGGGCTCGGTTCAACACCGTGTCCCGACGCTGGAGCGG 540
 Db |
 QY 531 CTGCTGTCTGTGTGTGCGAGGGCTCGGTTCAACACCGTGTCCCGACGCTGGAGCGG 590
 QY 541 GGGTTCAACAGCCAGCAGCGGGTGAACCTTGACCGTGAACGAGGGGAGCAGGTGCAGAG 600
 Db |
 QY 591 GGGTTCAACAGCCAGCAGCGGGTGAACCTTGACCGTGAACGAGGGGAGCAGGTGCAGAG 650
 QY 601 TGGGACAGGATCTCAAGCGCGCTTCAGTGGGCTGACCAACCCACCGCTGTGATCCCC 660
 Db |
 QY 651 TGGGACAGGATCTCAAGCGCGCTTCAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
 QY 661 GACATGACAGGCTTGCATCAAGGATAAGAAAGAGCAGCGAGGATCGTGGCGTGGTT 720
 Db |
 QY 711 GACATGACAGGCTTGCATCAAGGATAAGAAAGAGCAGCGAGGATCGTGGCGTGGTT 770
 QY 721 AAGAATCAAACTACTGCGCGTGC 744
 Db |
 QY 771 AAGAATCAAACTACTGCGCGTGC 794

RESULT 11

AA179867
 ID AA179867 standard; DNA; 1422 BP.

AC AA179867;

XX 25-MAR-2003 (updated)

DT 01-DEC-1997 (first entry)

DE Pro-ribosome inactivating protein gene clone RDT-G-A.

XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; ss.

OS Zea mays.

FX Key Location/Qualifiers

FT CDS 51..1259

XX /*tag= a

PN US5646026-A.

PD 08-JUL-1997.

XX 07-JUN-1995; 95US-0485286.

XX 09-DEC-1992; 92US-0987927.

PR 11-JUN-1990; 90US-0535636.

PR 26-JAN-1995; 95US-0378761.

PR 07-JUN-1995; 95US-0485286.

XX (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;

XX WPI; 1997-362934/33.
 DR P-PSDB; AAW25129.
 XX
 PT DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 PS Claim 2; Column 61-66; 186pp; English.
 XX
 CC AA179867 encodes a single chain maize pro-ribosome inactivating protein
 CC (proRIP) having a truncated leader sequence and carboxy terminus
 CC engineered for expression in Escherichia coli and which binds to
 CC immunoglobulin Igg. The construct has a sequence encoding the single
 CC antibody binding region (ABR) domains from Staphylococcus aureus
 CC antibody binding Protein A (ABR-A) and Streptococcus Group G protein
 CC G (ABR-G) inserted into a BamHI site. The sequence contains no
 CC linker separating the alpha and beta subunit regions and was shown
 CC to be a potent inhibitor of protein synthesis and bound specifically
 CC to Igg.
 CC proRIP sequences can be engineered to contain a selectively removable
 CC internal peptide linker sequence separating the alpha and beta units
 CC of the RIP protein to form an inactive form of RIP. When separated
 CC the two units regain activity and are capable of inactivating eukaryotic
 CC ribosomes and hence preventing protein production. Many different
 CC Panacoidae RIPs may be produced with an internal linker including:
 CC Barley Translation Inhibitor, Trichosanthin, Ricin A-chain, Abrin-A
 CC A-chain, Saporin, SLT-1, Luffin A, MAP, Ricinus communis agglutinin,
 CC Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in
 CC the construction of therapeutic toxins targeted to specific cells such
 CC as tumour cells via the attachment of a targeting polypeptide, e.g. a
 CC monoclonal antibody. A further use is in HIV therapy (see US4869903).
 CC There is interest in expressing RIP recombinantly in host eukaryotic
 CC cells, because of the capacity to provide correct post-translational
 CC processing. However, RIPs effectively inhibit protein synthesis in
 CC eukaryotic cells resulting in cell death. Since the proRIP proteins
 CC are not cytotoxic to eukaryotic cells, they can be recombinantly
 CC expressed in such cells and then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 1422 BP; 420 A; 364 C; 357 G; 281 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 1422;
 Best Local Similarity 99.7%; Pred. No. 6.9e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTCCAAAGTTCATGAAATCTCCCGTGAGAGACCGCAACTACCT 60

Db |
 51 ATGAAAGAAATAGTCCAAAGTTCATGAAATCTCCCGTGAGAGACCGCAACTACCT 110

QY 61 TACAGCGCTTCATCGCGTCCGCGGAAAGACGTGATCAAACTGCAACCGACCATATA 120

Db |
 111 TACAGCGCTTCATCGCGTCCGCGGAAAGACGTGATCAAACTGCAACCGACCATATA 170

QY 121 GGGATCTTCAGCCCGTGTGCTCCACCGGAGAAAGAGTCCCGGAGCTATGTTTACACA 180

Db |
 171 GGGATCTTCAGCCCGTGTGCTCCACCGGAGAAAGAGTCCCGGAGCTATGTTTACACA 230

QY 181 GAACTGAAACTAGGACAGCTCCATCAGCTCGGCATACGATCGGACAACTGTACCTC 240

Db |
 231 GAGCTCAAACTAGGACAGCTCCATCAGCTCGGCATACGATCGGACAACTGTACCTC 290

QY 241 GTGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTTCGGCAGGAGCGGACACCCAC 300

Db |
 291 GTGGCTTCAGGACCCCGGGGGGTGTGGTGGAGTTTCGGCAGGAGCGGACACCCAC 350

QY 301 CTCTTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACACGAGACTCATCGGC 360

Db |
 351 CTCTTCGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACACGAGACTCATCGGC 410

QY 361 AACAGGGTCTGGAGACCGTCAACATGGCGCGCCGAAATGACACAGGCGCTCAACGAC 420

Db |
 411 AACAGGGTCTGGAGACCGTCAACATGGCGCGCCGAAATGACACAGGCGCTCAACGAC 470

QY 421 CTGCGAAGAAGAAAGGGGGTGAACCCAGCCGACACGAAAGCAAGCTGGTGAAG 480
 DB 471 CTGCGAAGAAGAAAGGGGGTGAACCCAGCCGACACGAAAGCAAGCTGGTGAAG 530
 QY 481 CTGCTGTCTATGTTGCGAGGGCTGGGTTCAACACCGTGTCCGACGGTGGACGG 540
 DB 531 CTGCTGTCTATGTTGCGAGGGCTGGGTTCAACACCGTGTCCGACGGTGGACGG 590
 QY 541 GGGTTCAACAGCCAGCAGGGGGTCACTTGAACCGTGACGAGGGGAAGCAAGTGCAGAA 600
 DB 591 GGGTTCAACAGCCAGCAGGGGGTCACTTGAACCGTGACGAGGGGAAGCAAGTGCAGAA 650
 QY 601 TGGACAGGATCTCCAGGGGGCTTGCAGTGGGCTGACCAACCCACCGCTGTGATCCCC 660
 DB 651 TGGACAGGATCTCCAGGGGGCTTGCAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
 QY 661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGATCGTTGCGCTCGTT 720
 DB 711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGATCGTTGCGCTCGTT 770
 QY 721 AAGAAATCAAACTACTGCGCTGCC 744
 DB 771 AAGAAATCAAACTACTGCGCTGCC 794

RESULT 12

AAT77759
 ID AAT77759 standard; DNA; 1422 BP.
 AC AAT77759;
 XX AAT77759;
 DT 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 DE RIP fusion protein, RDT-G-A coding sequence.
 XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX Synthetic.
 FH Key Location/Qualifiers
 FT 51..1256
 FT CDS /tag= a
 FT /product= RDT-G-A
 XX
 PN US5635384-A.
 XX
 PD 03-JUN-1997.
 XX
 PF 26-JAN-1995; 95US-0378761.
 XX
 PR 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 PA (DOW) DOWELANCO.
 XX
 PI Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-309831/28.
 DR P-PSDB; AAW21716.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 PT internal linker sequences
 XX
 PS Claim 4; Column 61-64; 121pp; English.
 XX
 XX The sequences given in AAT77754-63 encode fusion proteins which are

CC examples of Ribosome Inactivating Proteins. RIPS are potent inhibitors
 CC of eukaryotic protein synthesis. They possess a highly specific
 CC N-glycosidase activity which cleaves the glycosidic bond of adenine
 CC 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
 CC cellular proliferation of cells, e.g. cancer cells and HIV-infected
 CC T cells. The inactive proRIP proteins make it possible to provide
 CC protein synthesis inhibitors with uses in practical and improved
 CC ways not before possible. The RIP can be used to make cytotoxic
 CC conjugates.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 1422 BP; 420 A; 364 C; 357 G; 281 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 1422;
 Best Local Similarity 99.7%; Pred. No. 6.9e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAGAAATAGTCCCAAGTTCACTGAATCTTCCCGTGGAGGACCGAACTACCCCT 60
 DB 51 ATGAAAGAAATAGTCCCAAGTTCACTGAATCTTCCCGTGGAGGACCGAACTACCCCT 110
 QY 61 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAAACTACGACCGACATAAA 120
 DB 111 TACAGCGCTTCATCGCTCGGTCCGGAAGACGTGATCAAACTACGACCGACATAAA 170
 QY 121 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGAGCTATGTTCTACACA 180
 DB 171 GGGATCTTCCAGCCCGTCTGCCACCGAGAGAGGTCCCGAGCTATGTTCTACACA 230
 QY 181 GAATGAAATAGGACCGAGCTCCATCAGCTTCGCTATACATGGAACAACTGATCCTC 240
 DB 231 GAGCTCAAAATAGGACCGAGCTCCATCAGCTTCGCTATACATGGAACAACTGATCCTC 290
 QY 241 GTGGCTTCAGACCCCGGGGGGTGTGGTGGAGTTCGCAAGAGGCGGACACCCAC 300
 DB 291 GTGGCTTCAGACCCCGGGGGGTGTGGTGGAGTTCGCAAGAGGCGGACACCCAC 350
 QY 301 CTCCTCGGCGACAACCCAGGTGGCTTCGGCTTCGGCGGAGTACCGAGCTCATCGGC 360
 DB 351 CTCCTCGGCGACAACCCAGGTGGCTTCGGCTTCGGCGGAGTACCGAGCTCATCGGC 410
 QY 361 AACAGGGTCTGGAGACCGTACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGAC 420
 DB 411 AACAGGGTCTGGAGACCGTACCATGGGCGCGCGGAAATGACAGGCGCGTCAACGAC 470
 QY 421 CTGGCGAAGAAAGAGCGGCTGACCCACAGGCGCGACAGCAAGCAAGCTGTGAAG 480
 DB 471 CTGGCGAAGAAAGAGCGGCTGACCCACAGGCGCGACAGCAAGCAAGCTGTGAAG 530
 QY 481 CTGGTGGTTCATGTTGCGAGGGGTGCGGTTCAACACCGTGTCCCGACGGTGACGCG 540
 DB 531 CTGGTGGTTCATGTTGCGAGGGGTGCGGTTCAACACCGTGTCCCGACGGTGACGCG 590
 QY 541 GGGTTCAACAGCCAGCAGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAA 600
 DB 591 GGGTTCAACAGCCAGCAGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAA 650
 QY 601 TGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGTGACCAACCCACCGCTGTGATCCCC 660
 DB 651 TGGGACAGGATCTCCAAGCGCGCTTCGAGTGGGTGACCAACCCACCGCTGTGATCCCC 710
 QY 661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGATCGTTGCGCTCGTT 720
 DB 711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGCAGGAGATCGTTGCGCTCGTT 770
 QY 721 AAGAAATCAAACTACTGCGCTGCC 744
 DB 771 AAGAAATCAAACTACTGCGCTGCC 794

RESULT 13

AAQ20482
 ID AAQ20482 standard; DNA; 1683 BP.

XX AAQ20482;
 AC
 XX
 DT 13-APR-1992 (first entry)
 XX
 DE Maize RIP deriv. RDT-G-G-A.
 XX
 KW Ribosome-inactivating protein; alpha RIP; beta RIP; alpha-beta RIP;
 KW HIV; tumour; IgG; immunoglobulin; protein G;
 KW antibody binding domain; ABR; ss.
 XX
 OS
 XX
 XX Key Location/Qualifiers
 XX CDS 51..1520
 FT /*tag= a
 FT /label= RDT-G-G-A
 FT /note= "RIP deriv."
 XX
 XX EP466222-A.
 PN
 XX
 XX 15-JAN-1992.
 PD
 XX
 XX 10-JUN-1991; 91EP-0201436.
 PF
 XX
 XX 11-JUN-1990; 90US-0535636.
 PR
 XX
 XX (DOWC) DOWELANCO.
 PA
 XX
 XX Walsh TA, Hey TD, Morgan AER;
 PI
 XX
 DR WPI; 1992-017847/03.
 DR P-PSDB; AAR20085.
 XX
 XX New plant ribosome inactivating proteins and inactive precursors
 PT - expressed in eukaryotic cells, useful e.g. in tumour or HIV
 PT treatment, and new DNA encoding them
 PT
 XX
 PS Disclosure; Page 32-33; 40pp; English.
 XX
 XX To increase to binding ability of the RDT-A (AAQ20480) to IgG
 CC antibody binding domain from Streptococcal group G protein G
 CC (ABR-G) was synthesised using oligonucleotides. The ABR-G fragment
 CC was inserted into the BamHI site of RDT-A. Two classes of clones
 CC have been studied. RDT-G-A contains a single ABR-G domain inserted
 CC in the correct orientation between the 3' end of RDT and the 5' end
 CC of ABR-A (AAQ20481). A second class contains two properly oriented
 CC of ABR-G domains (AAQ20482).
 CC See also AAQ20476-82.
 XX
 XX Sequence 1683 BP; 513 A; 423 C; 408 G; 339 T; 0 other;
 SQ
 Query Match 98.8%; Score 740.8; DB 13; Length 1683;
 Best Local Similarity 99.7%; Pred. No. 7.1e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAAAAGATAGTCCAAAGTTCACTGAAATCTTCCCGGTGGAGGACGCAACTACCT 60
 DB 51 ATGAAAAGATAGTCCAAAGTTCACTGAAATCTTCCCGGTGGAGGACGCAACTACCT 110
 QY 61 TACAGCGCTTCATCGCGTCGGTCCGGAAGACGTGATCAACACTGACCGACCATAAA 120
 DB 111 TACAGCGCTTCATCGCGTCGGTCCGGAAGACGTGATCAACACTGACCGACCATAAA 170
 QY 121 GGGATCTTCCAGCCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTTACACA 180
 DB 171 GGGATCTTCCAGCCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTTACACA 230
 QY 181 GAACTGAAACTAGGACCACTGCTCAGCTCGGCATACGATGGAACAACCTGTACCTC 240
 DB 231 GAGCTCAAAACTAGGACCACTGCTCAGCTCGGCATACGATGGAACAACCTGTACCTC 290
 QY 241 GTGGGCTTCAGGACCCCGGGCGGGTGTGGTGGAGTTTCGGCAAGGACGGCGACCCAC 300

DB 291 GTGGGCTTCAGGACCCCGGGCGGGTGTGGTGGAGTTTCGCAAGGACGGCGACCCAC 350
 QY 301 TTCTTCGGCGCAACACCCAGGTGGCTGGCTTCGGCGGACGTACCAAGGACCTCATCGGC 360
 DB 351 TTCTTCGGCGCAACACCCAGGTGGCTGGCTTCGGCGGACGTACCAAGGACCTCATCGGC 410
 QY 361 AACAGGCTCTGGAGACCGTCAACATGGCGCGCCGAAATGACAGGCGCGTCAACGAC 420
 DB 411 AACAGGCTCTGGAGACCGTCAACATGGCGCGCCGAAATGACAGGCGCGTCAACGAC 470
 QY 421 CTGGCGAAAGAGAGAGAGCGCGCTGACCCACAGGCGCGACAGAGAGCAAGCTGTGAAG 480
 DB 471 CTGGCGAAAGAGAGAGAGCGCGCTGACCCACAGGCGCGACAGAGAGCAAGCTGTGAAG 530
 QY 481 CTGGTGGTCAATGGTGTGGAGGGGTGGCTTCAACACCGTGTCCGACCGTGGACGCG 540
 DB 531 CTGGTGGTCAATGGTGTGGAGGGGTGGCTTCAACACCGTGTCCGACCGTGGACGCG 590
 QY 541 GGGTTCAACAGCAGCAGCGGGTGAACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAA 600
 DB 591 GGGTTCAACAGCAGCAGCGGGTGAACCTTGACCGTGAACGAGGGAAGCAGGTGCAGAA 650
 QY 601 TGGGACAGGATCTCAAGCGCGCTTCGAGTGGGTGACACCCACCGCTGTGATCCCC 660
 DB 651 TGGGACAGGATCTCAAGCGCGCTTCGAGTGGGTGACACCCACCGCTGTGATCCCC 710
 QY 661 GACATGCAGAACTTGGCATCAAGGATAAGAACAGCAGCAGGATCGTTGGCTCGTT 720
 DB 711 GACATGCAGAACTTGGCATCAAGGATAAGAACAGCAGCAGGATCGTTGGCTCGTT 770
 QY 721 AAGAATCAAACTACTGCCGCTGCC 744
 DB 771 AAGAATCAAACTACTGCCGCTGCC 794
 RESULT 14
 AAT79868
 ID AAT79868 standard; DNA; 1683 BP.
 XX
 AC AAT79868;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-DEC-1997 (first entry)
 XX
 XX Pro-ribosome inactivating protein gene clone RDT-G-G-A.
 XX
 KW Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; ss.
 XX
 OS Zea mays.
 XX
 XX Key Location/Qualifiers
 XX CDS 51..1520
 FT /*tag= a
 XX
 XX US5646026-A.
 PN
 XX
 PD 08-JUL-1997.
 XX
 XX 07-JUN-1995; 95US-0485286.
 XX
 XX 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 28-JAN-1995; 95US-0378761.
 PR 07-JUN-1995; 95US-0485286.
 XX
 PA (DOWC) DOWELANCO.

XX Hey TD, Morgan AER, Walsh TA;
 PI WPI; 1997-362934/33.
 DR P-PSDB; AAW25130.
 XX
 XX DNA encoding pro-ribosome inactivating proteins - inactive
 PT precursors of ribosome inactivating proteins; can be expressed in
 PT eukaryotic cells without causing cell death
 XX
 PS Claim 2; Column 67-72; 186pp; English.
 XX
 CC AAT79868 encodes a single chain maize pro-ribosome inactivating protein
 CC (proRIP) having a truncated leader sequence and carboxy terminus
 CC engineered for expression in *Escherichia coli* and which binds to
 CC immunoglobulin IgG. The construct has a sequence encoding the single
 CC antibody binding region (ABR) domain from *Staphylococcus aureus*
 CC antibody binding Protein A (ABR-A) and two Streptococcal Group G
 CC protein G (ABR-G) polypeptides inserted into a BamHI site. The
 CC sequence contains no linker separating the alpha and beta subunit
 CC regions and was shown to be a potent inhibitor of protein synthesis
 CC and bound specifically to IgG.
 CC proRIP sequences can be engineered to contain a selectively removable
 CC internal peptide linker sequence separating the alpha and beta units
 CC of the RIP protein to form an inactive form of RIP. When separated
 CC the two units regain activity and are capable of inactivating eukaryotic
 CC ribosomes and hence preventing protein production. Many different
 CC Panacoidae RIPs may be produced with an internal linker including:
 CC Barley translation inhibitor, Itrichosanthin, Ricin A-chain, Abrin-A
 CC A-chain, Saporin, SRT-1, Luffin A, MAP, Ricinus communis agglutinin,
 CC Momordin, PAP-S, Luffin-B and Dianthin 30. The RIPs can be used in
 CC the construction of therapeutic toxins targeted to specific cells such
 CC as tumour cells via the attachment of a targeting polypeptide, e.g. a
 CC monoclonal antibody. A further use is in HIV therapy (see US4869903).
 CC There is interest in expressing RIP recombinantly in host eukaryotic
 CC cells, because of the capacity to provide correct post-translational
 CC processing. However, RIPs effectively inhibit protein synthesis in
 CC eukaryotic cells resulting in cell death. Since the proRIP proteins
 CC are not cytotoxic to eukaryotic cells, they can be recombinantly
 CC expressed in such cells and then converted to active RIP proteins.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 1683 BP; 513 A; 419 C; 412 G; 339 T; 0 other;

Query Match 98.8%; Score 740.8; DB 18; Length 1683;
 Best Local Similarity 99.7%; Pred. No. 7.1e-148;
 Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAAGAAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGGCGGAACCTACCT 60
 DB 51 ATGAAAGAAATAGTCCAAAGTTCACTGAATCTTCCCGTGGAGGCGGAACCTACCT 110
 QY 61 TACAGCGCTTCATCGCGTCCGGTCCGGAAGAGCGTGATCAACACCTGACCGACCAATAA 120
 DB 111 TACAGCGCTTCATCGCGTCCGGTCCGGAAGAGCGTGATCAACACCTGACCGACCAATAA 170
 QY 121 GGGATCTTCCAGCCCGTGTGTCACCGAGAGAGAGTCCCGAGCTATGTTCTACACA 180
 DB 171 GGGATCTTCCAGCCCGTGTGTCACCGAGAGAGAGTCCCGAGCTATGTTCTACACA 230
 QY 181 GAACCTGAAACCTPAGGACAGCTCCATCAGCTCGCCATACGATGGACCACTGTACCTC 240
 DB 231 GAGCTCAAACTAGGACCAAGCTTCATCAGCTCGCCATACGATGGACCACTGTACCTC 290
 QY 241 GTGGGCTTCAGGACCCCGCGGGGTGTGTGGAGTTTCGGAAGACGGCGACACCCAC 300
 DB 291 GTGGGCTTCAGGACCCCGCGGGGTGTGTGGAGTTTCGGAAGACGGCGACACCCAC 350
 QY 301 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCGCGGCGAGTACCAAGACCTCATCGGC 360
 DB 351 CTCCTCGGCGACAAACCCAGGTGGCTCGGCTTCGCGGCGAGTACCAAGACCTCATCGGC 410
 QY 361 AACAGGGGTCTGAGAGACCGTCAACCATGGGCGCGCGAAATGACCGGGCGGTCAACGAC 420

DB 411 AACAGGGGTCTGAGAGACCGTCAACATGGGCGCGCGAAATGACCGGGCGGTCAAACGAC 470
 QY 421 CTGGCGAAAGAAAGAAAGCGGCTGACCCACAGCCCGACACGAAGAGCAAGCTGGTGAAG 480
 DB 471 CTGGCGAAAGAAAGAAAGCGGCTGACCCACAGCCCGACACGAAGAGCAAGCTGGTGAAG 530
 QY 481 CTGGTGGTCTATGTTGTGGAGGGCTGCGGTTCAACACCGTGTCCGACCGTGGACGCG 540
 DB 531 CTGGTGGTCTATGTTGTGGAGGGCTGCGGTTCAACACCGTGTCCGACCGTGGACGCG 590
 QY 541 GGGTTCAACAGCCAGCCAGCGGGTGACCTTGACCGTGGAGCGAGGGAAGACAGTGCAGAA 600
 DB 591 GGGTTCAACAGCCAGCCAGCGGGTGACCTTGACCGTGGAGCGAGGGAAGACAGTGCAGAA 650
 QY 601 TGGGACAGGATCTCAAGCGCGGCTTCGAGTGGGCTGACCGACCGCCCGCTGTGATCCCC 660
 DB 651 TGGGACAGGATCTCAAGCGCGGCTTCGAGTGGGCTGACCGACCGCCCGCTGTGATCCCC 710
 QY 661 GACATGCGAAGCTTGGCATCAAGGATAAGAAACGAAGCAGCGAGGATCGTTGGCGTCTGT 720
 DB 711 GACATGCGAAGCTTGGCATCAAGGATAAGAAACGAAGCAGCGAGGATCGTTGGCGTCTGT 770
 QY 721 AAGAATCAAACTACTGCGCGTGC 744
 DB 771 AAGAATCAAACTACTGCGCGTGC 794

RESULT 15
 AAT77760
 ID AAT77760 standard; DNA; 1683 BP.
 XX
 AC AAT77760;
 XX
 DT 25-MAR-2003 (updated)
 DT 26-SEP-1997 (first entry)
 XX
 DE RIP fusion protein, RDT-G-GA coding sequence.
 KW pro-Ribosome inactivating Protein; proRIP; peptide linker; cancer;
 KW inactivator; eukaryotic ribosome; alpha fragment; beta fragment;
 KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
 KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell; ss.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT CDS 51..1520
 FT /*tag= a
 FT /product= RDT-G-GA
 XX
 PN US5635384-A.
 XX
 PD 03-JUN-1997.
 XX
 PF 26-JAN-1995; 95US-0378761.
 XX
 PR 09-DEC-1992; 92US-0987927.
 PR 11-JUN-1990; 90US-0535636.
 PR 26-JAN-1995; 95US-0378761.
 XX
 PA (DOWC) DOWELANCO.
 XX
 PI Hey TD, Morgan AER, Walsh TA;
 XX
 DR WPI; 1997-309831/28.
 DR P-PSDB; AAW21717.
 XX
 PT Inactive precursor of maize ribosome-inactivating protein - also
 PT chimeric ribosome-inactivating protein precursors containing
 XX internal linker sequences
 PS Claim 4; Column 67-70; 121pp; English.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 22, 2003, 04:23:14, Search time 2892 Seconds
(without alignments)
10609.343 Million cell updates/sec

Title: US-09-978-273-2

Perfect score: 750

Sequence: 1 atgaaagaatagtgccaaa.....ctactgcgcgtgcctaataa 750

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.on.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.on.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pin.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	750	100.0	750	6	AX427661	AX427661 Sequence
2	740.8	98.8	847	6	I44710	I44710 Sequence 20
3	740.8	98.8	847	6	I52116	I52116 Sequence 20
4	740.8	98.8	978	6	I44705	I44705 Sequence 10
5	740.8	98.8	978	6	I52111	I52111 Sequence 10
6	740.8	98.8	985	6	I44704	I44704 Sequence 8
7	740.8	98.8	985	6	I52110	I52110 Sequence 8
8	740.8	98.8	1161	6	I44707	I44707 Sequence 14
9	740.8	98.8	1161	6	I52113	I52113 Sequence 14
10	740.8	98.8	1422	6	I44708	I44708 Sequence 16
11	740.8	98.8	1422	6	I52114	I52114 Sequence 16
12	740.8	98.8	1683	6	I44709	I44709 Sequence 18
13	740.8	98.8	1683	6	I52115	I52115 Sequence 18
14	740.8	98.8	1695	6	I44711	I44711 Sequence 22
15	740.8	98.8	1695	6	I52117	I52117 Sequence 22
16	740.8	98.8	1722	6	I44712	I44712 Sequence 24
17	740.8	98.8	1722	6	I52118	I52118 Sequence 24
18	737.8	98.4	1029	6	I44703	I44703 Sequence 6
19	737.8	98.4	1029	6	I52109	I52109 Sequence 6
20	720.2	96.0	987	6	I44706	I44706 Sequence 12
21	720.2	96.0	987	6	I52112	I52112 Sequence 12
22	707.2	94.3	987	6	AR123360	AR123360 Sequence
23	656	87.5	909	6	AX427660	AX427660 Sequence
24	655.8	87.4	1074	6	I44702	I44702 Sequence 4
25	655.8	87.4	1074	6	I52108	I52108 Sequence 4
26	654.2	87.2	1059	6	AR123363	AR123363 Sequence
27	652.8	87.0	1076	6	I44700	I44700 Sequence 1
28	652.8	87.0	1076	6	I52106	I52106 Sequence 1
29	652.8	87.0	1076	6	MZERIP	M7122 Z.mays ribo
30	652.8	87.0	1105	6	I44701	I44701 Sequence 3
31	652.8	87.0	1105	6	I52107	I52107 Sequence 3
32	652.6	87.0	1053	6	AR123366	AR123366 Sequence
33	649.8	86.6	944	6	AR123368	AR123368 Sequence
34	649.8	86.6	1244	6	AR123372	AR123372 Sequence
35	644.2	85.9	1039	8	MZERIP3A	M83926 Zea mays ri
36	638.4	85.1	1826	8	ZMB32152	X70154 Z.mays mRNA
37	636.8	84.9	1245	6	AR123374	AR123374 Sequence
38	632.2	84.3	976	8	MZERIP9A	M83927 Zea mays ri
39	628.8	83.8	959	8	ZMA300265	AJ300265 Zea mays
40	627.4	83.7	2741	8	ZMB32129	X70153 Z.mays mRNA
41	607.6	81.0	3093	8	ZMB32120	X54212 Z.mays mRNA
42	606	80.8	1044	8	ZMALBB32	X07987 Maize mRNA
43	521.4	69.5	983	8	AF233881	AF233881 Zea mays
44	510.8	68.1	963	8	MZERIP2A	L26305 Zea mays ri
45	510.8	68.1	1934	6	I25465	I25465 Sequence 1

ALIGNMENTS

RESULT 1
AX427661
LOCUS AX427661 750 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 2 from Patent WO0233106.
ACCESSION AX427661
VERSION AX427661.1 GI:21537780
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS Neelam.A., Atkinson.H.J., Mcpherson.M.J. and Thomas.C.J.R.
TITLE Plant cell death system


```
Db      591 GGGTTCAACAGCCAGCAAGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 650
QY      601 TGGGACAGGATCTCCAAAGGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 660
Db      651 TGGGACAGGATCTCCAAAGGGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
QY      661 GACATGACAGAGCTTGGCATCAAGGATAAGAAACGAAGCAGGAGATCGTTGGCGTCGTT 720
Db      711 GACATGACAGAGCTTGGCATCAAGGATAAGAAACGAAGCAGGAGATCGTTGGCGTCGTT 770
QY      721 AAGAATCAAACTACTGCGCGTGCC 744
Db      771 AAGAATCAAACTACTGCGCGTGCC 794

RESULT 5
LOCUS      152111
DEFINITION Sequence 10 from patent US 5646026.
ACCESSION 152111
VERSION    152111.1 GI:2473312
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 978)
AUTHORS    Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE      Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL    Patent: US 5646026-A 10 08-JUL-1997;
FEATURES   Location/Qualifiers
            source
            1..978
            /organism="unknown"
BASE COUNT 250 a 271 c 275 g 182 t
ORIGIN

Query Match      98.8%; Score 740.8; DB 6; Length 978;
Best Local Similarity 99.7%; Pred. No. 3.1e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATGAAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 60
Db      51 ATGAAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 110
QY      61 TACAGCGCCTTCATCGCGTCGGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 120
Db      111 TACAGCGCCTTCATCGCGTCGGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 170
QY      121 GGGATCTTCCAGCCGTGTGCCACCGGAGAGAGAGTCCCGAGGATATGGTTCTACACA 180
Db      171 GGGATCTTCCAGCCGTGTGCCACCGGAGAGAGAGTCCCGAGGATATGGTTCTACACA 230
QY      181 GAATCAAAATAGGACCAAGCTCCATCAAGCTCGCCATACGATGACAACTGTACCTC 240
Db      231 GAGCTCAAAATAGGACCAAGCTCCATCAAGCTCGCCATACGATGACAACTGTACCTC 290
QY      241 GTGGGTTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 300
Db      291 GTGGGTTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 350
QY      301 CTCCTCGGCGACACCCCGAGGTGGCTCGGCTTCGGGGGAGGTACAGGACCTCATCGGC 360
Db      351 CTCCTCGGCGACACCCCGAGGTGGCTCGGCTTCGGGGGAGGTACAGGACCTCATCGGC 410
QY      361 AACAGGGTCTGGAGACCGCTCAATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 420
Db      411 AACAGGGTCTGGAGACCGCTCAATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 470
QY      421 CTGGCGAAGAAAGAGCGGCTGACCAAGGCGGACACGAGGAGCAAGCTGGTGAAG 480
Db      471 CTGGCGAAGAAAGAGCGGCTGACCAAGGCGGACACGAGGAGCAAGCTGGTGAAG 530
QY      481 CTGGTGGTTCATGGTGTGGAGGGGTGCGGTTCAACACCGTGTCCCGCACGCGTGACGCG 540
```

```
Db      531 CTGGTGGTTCATGTGTGGAGGGGCTCGGTTCAACACCGTGTCCCGCACCGTGGAGCGG 590
QY      541 GGGTTCAACAGCCAGCAGCGGGTGAACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 600
Db      591 GGGTTCAACAGCCAGCAGCAGCGGGTGAACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 650
QY      601 TGGGACAGGATCTCCAAAGCGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 660
Db      651 TGGGACAGGATCTCCAAAGCGCGCTTCGAGTGGGCTGACCAACCCACCGCTGTGATCCCC 710
QY      661 GACATCAGAGCTTGGCATCAAGGATAAGAAACGAAGCAGGAGATCGTTGGCGTCGTT 720
Db      711 GACATCAGAGCTTGGCATCAAGGATAAGAAACGAAGCAGGAGATCGTTGGCGTCGTT 770
QY      721 AAGAATCAAACTACTGCGCGTGCC 744
Db      771 AAGAATCAAACTACTGCGCGTGCC 794

RESULT 6
LOCUS      144704
DEFINITION Sequence 8 from patent US 5635384.
ACCESSION 144704
VERSION    144704.1 GI:2469417
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 985)
AUTHORS    Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
TITLE      Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL    Patent: US 5635384-A 8 03-JUN-1997;
FEATURES   Location/Qualifiers
            source
            1..985
            /organism="unknown"
BASE COUNT 255 a 271 c 279 g 180 t
ORIGIN

Query Match      98.8%; Score 740.8; DB 6; Length 985;
Best Local Similarity 99.7%; Pred. No. 3.1e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ATGAAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 60
Db      37 ATGAAAAGAAATAGTGCACAAAGTTCACTGAAATCTTCCCGTGGAGACGCGAACTACCTT 96
QY      61 TACAGCGCCTTCATCGCGTCGGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 120
Db      97 TACAGCGCCTTCATCGCGTCGGTCCGGAAGAGCGTGATCAAACTGCACCGACCAATAA 156
QY      121 GGGATCTTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 180
Db      157 GGGATCTTCCAGCCGTGTGCCACCGGAGAGAGGTCCCGAGCTATGGTTCTACACA 216
QY      181 GAATCAAAATAGGACCAAGCTCCATCAAGCTCGCCATACGATGACAACTGTACCTC 240
Db      217 GAGCTCAAAATAGGACCAAGCTCCATCAAGCTCGCCATACGATGACAACTGTACCTC 276
QY      241 GTGGGTTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 300
Db      277 GTGGGTTTCAGGACCCCGGGGGGTGTGGTGGAGTTCGGCAAGACGCGGACACCCAC 336
QY      301 CTCCTCGGCGACACCCCGAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
Db      337 CTCCTCGGCGACACCCCGAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 396
QY      361 AACAGGGTCTGGAGACCGCTCACCATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 420
Db      397 AACAGGGTCTGGAGACCGCTCACCATGGGCCCGCGGAATGACAGGCGCGTCAACGAC 456
```

361	QY	AACGAGGGTCTGGAGACCGCTCACATGCGGCGCGCGGAATGACGAGGGCGGTCAACGAC	420
362	QY		
363	QY		
364	QY		
365	QY		
366	QY		
367	DB	AACGAGGGTCTGGAGACCGCTCACATGCGGCGCGCGGAATGACGAGGGCGGTCAACGAC	456
368	DB		
369	DB		
370	DB		
371	DB		
372	DB		
373	DB		
374	DB		
375	DB		
376	DB		
377	DB		
378	DB		
379	DB		
380	DB		
381	QY	CTGTGGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCGCAACCGTGGACGCG	540
382	QY		
383	QY		
384	QY		
385	QY		
386	QY		
387	DB	CTGTGGTTCATGTGTGCGAGGGGCTGCGGTTCAACACCGTGTCCGCAACCGTGGACGCG	576
388	DB		
389	DB		
390	DB		
391	DB		
392	DB		
393	DB		
394	DB		
395	DB		
396	DB		
397	DB		
398	DB		
399	DB		
400	DB		
401	QY	GGGTTCAACAGCAGACGCGGGGTGACCTTTGACCGTGAACGAGGGGAACGAGTGCAGAG	600
402	QY		
403	DB	GGGTTCAACAGCAGCAGCGGGGTGACCTTTGACCGTGAACGAGGGGAACGAGTGCAGAG	636
404	DB		
405	DB		
406	DB		
407	QY	TGGGACAGGATCTCCAAAGCGGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC	660
408	QY		
409	DB	TGGGACAGGATCTCCAAAGCGGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC	696
410	DB		
411	DB		
412	DB		
413	DB		
414	DB		
415	QY	GACATGCAGAGAGTTGGCATCAAGGTAAGAAACGAAGCAGCAGGAGATCGTTCGCTCGTT	720
416	QY		
417	DB	GACATGCAGAGAGTTGGCATCAAGGTAAGAAACGAAGCAGCAGGAGATCGTTCGCTCGTT	756
418	DB		
419	DB		
420	DB		
421	QY	AAGAAATCAAACCTACTCGCGCTGCC	744
422	QY		
423	QY		
424	QY		
425	QY		
426	DB	AAGAAATCAAACCTACTCGCGCTGCC	780
427	DB		
428	DB		
429	DB		
430	DB		

RESULT 8				
I44707				
LOCUS				
DEFINITION	I44707	1161 bp	DNA	
ACCESSION	I44707	Sequence 14 from patent US 5635384.		linear PAT 07-OCT-1997
VERSION	I44707.1	GI:2469420		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	Walsh, T.A., Hey, T.D. and Morgan, A.E.R.			
TITLE	Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using			
JOURNAL	Patent: US 5635384-A 14 03-JUN-1997;			

Query Match	98.8%;	Score 740.8;	DB 6;	Length 1161;
Best Local Similarity	99.7%;	Pred. No. 3e-103;		
Matches 742;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	ATGAAAAGATAGTGC	CGAAGTTCAC	TGAAATCTCCCGTCGGAGACGGCACTACCCCT 60
DB	51	ATGAAAAGATAGTGC	CGAAGTTCAC	TGAAATCTCCCGTCGGAGACGGCACTACCCCT 110
QY	61	TACAGCGCCTTCATCG	CGCTCGGTCGGAAAGACGTGATCAAACTGTCACCGCACATAAA 120	
DB	111	TACAGCGCCTTCATCG	CGCTCGGTCGGAAAGACGTGATCAAACTGTCACCGCACATAAA 170	
QY	121	GGGATCTTCCAGCCG	TGCTGCCACCGAGAGAGGTC	CCGGAGCTATGTTGTTTACACAA 180
DB	171	GGGATCTTCCAGCCG	TGCTGCCACCGAGAGAGGTC	CCGGAGCTATGTTGTTTACACAA 230
QY	181	GAACTGAAAACTGGAC	CCAGCTCCATCAGCTCGCCATAGCATGGACAACCTGCTGACCTC 240	
DB	231	GAGCTCAAAACTGGAC	CCAGCTCCATCAGCTCGCCATAGCATGGACAACCTGCTGACCTC 290	
QY	241	GTGGGCTTTCAGAGCC	CGGCGGGGTGTGTTGGGAGTTGCGCAAGGACGGCGACACCCAC 300	

```

Db      291 GTGGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGACGCGGACACCCAC 350
Qy      301 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACAGGACCTCATCGGC 360
Db      351 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACAGGACCTCATCGGC 410
Qy      361 AACAGGCTCTGGAGACCGTCACCATGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 420
Db      411 AACAGGCTCTGGAGACCGTCACCATGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 470
Qy      421 CTGGCAAGAAAGAAAGGCGGCTGACCCACAGGCGGCGGACGAGAGCAAGTGGTGAAG 480
Db      471 CTGGCAAGAAAGAAAGGCGGCTGACCCACAGGCGGCGGAAATGACCAAGGCGCGTGGTGAAG 530
Qy      481 CTGGTGTCTATGGTGTGGAGGGGCTGGGTTCAACCGTGTCCCGCACGGTGGACGG 540
Db      531 CTGGTGTCTATGGTGTGGAGGGGCTGGGTTCAACCGTGTCCCGCACGGTGGACGG 590
Qy      541 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGCAAGTGGCAAG 600
Db      591 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGCAAGTGGCAAG 650
Qy      601 TGGGACAGGACTCCAAAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Db      651 TGGGACAGGACTCCAAAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
Qy      661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 720
Db      711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 770
Qy      721 AAGAACTCAAACTACTGCGCGTGC 744
Db      771 AAGAACTCAAACTACTGCGCGTGC 794

RESULT 9
LOCUS      152113
DEFINITION Sequence 14 from patent US 5646026.
ACCESSION 152113
VERSION    152113.1 GI:2473314
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1161)
AUTHORS    Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
TITLE      Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL     Patent: US 5646026-A 14 08-JUL-1997;
FEATURES    Location/Qualifiers
            source
BASE COUNT 327 a 309 c 302 g 223 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 1161;
Best Local Similarity 99.7%; Pred. No. 3e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 60
Db      51 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 110
Qy      61 TACAGCGCTTCATCGCGTGGTCCGAAAGACGATGATCAAAACACTGACCGACCATATAA 120
Db      111 TACAGCGCTTCATCGCGTGGTCCGAAAGACGATGATCAAAACACTGACCGACCATATAA 170
Qy      121 GGGATCTCCAGCCGCTGTCACCGGAGAGAGGTCGCGGAGCTATGCTTCTACACA 180
Db      171 GGGATCTCCAGCCGCTGTCACCGGAGAGAGGTCGCGGAGCTATGCTTCTACACA 230
Qy      181 GAACTGAAACTAGGACCACTCCATCAGCTCGCCATACGATGGACAACTGTACTC 240

```

```

Db      231 GAGCTCAAAATAGGACACAGCTCCATCAGCTCCGCTACGATCGCATGGACACCTGTACTC 290
Qy      241 GTGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGGACGCGGACACCCAC 300
Db      291 GTGGCTTCAGGACCCCGGGGGTGTGGTGGAGTTTCGGCAAGGACGCGGACACCCAC 350
Qy      301 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACAGGACCTCATCGGC 360
Db      351 CTCTCCGGCGACACACCCAGGTGGCTCGGCTTCGGCGGCGAGGTACAGGACCTCATCGGC 410
Qy      361 AACAGGCTCTGGAGACCGTCACCATGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 420
Db      411 AACAGGCTCTGGAGACCGTCACCATGGCGCGCGGAAATGACCAAGGCGCGTCAACGAC 470
Qy      421 CTGGCAAGAAAGAAAGGCGGCTGACCCACAGGCGGCGGAAATGACCAAGGCGCGTGGTGAAG 480
Db      471 CTGGCAAGAAAGAAAGGCGGCTGACCCACAGGCGGCGGAAATGACCAAGGCGCGTGGTGAAG 530
Qy      481 CTGGTGTCTATGGTGTGGAGGGGCTGGGTTCAACCGTGTCCCGCACGGTGGACGG 540
Db      531 CTGGTGTCTATGGTGTGGAGGGGCTGGGTTCAACCGTGTCCCGCACGGTGGACGG 590
Qy      541 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGCAAGTGGCAAG 600
Db      591 GGGTTCAACAGCAGCAGCGGGTCACTTGACCGTGAACGAGGAGCAAGTGGCAAG 650
Qy      601 TGGGACAGGACTCCAAAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660
Db      651 TGGGACAGGACTCCAAAGGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710
Qy      661 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 720
Db      711 GACATGCAGAGCTTGGCATCAAGGATAAGAAACGAGGAGGATCGTTGCGCTCGTT 770
Qy      721 AAGAACTCAAACTACTGCGCGTGC 744
Db      771 AAGAACTCAAACTACTGCGCGTGC 794

RESULT 10
LOCUS      144708
DEFINITION Sequence 16 from patent US 5635384.
ACCESSION 144708
VERSION    144708.1 GI:2469421
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1422)
AUTHORS    Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
TITLE      Ribosome-inactivating proteins, inactive precursor forms thereof, a
            process for making and a method of using
JOURNAL     Patent: US 5635384-A 16 03-JUN-1997;
FEATURES    Location/Qualifiers
            source
BASE COUNT 420 a 364 c 357 g 281 t
ORIGIN

Query Match 98.8%; Score 740.8; DB 6; Length 1422;
Best Local Similarity 99.7%; Pred. No. 2.9e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 60
Db      51 ATGAAAGAAATAGTCCAAAGTTCACTGAAATCTTCCCGTGGAGGACGGCACTACCT 110
Qy      61 TACAGCGCTTCATCGCGTGGTCCGAAAGACGATGATCAAAACACTGACCGACCATATAA 120
Db      111 TACAGCGCTTCATCGCGTGGTCCGAAAGACGATGATCAAAACACTGACCGACCATATAA 170

```

```
QY 121 GGGATCTTCAGCCCGGTGCTGCCACCGAGAGAGAGTCCCGGAGCTATGGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGGTGCTGCCACCGAGAGAGAGTCCCGGAGCTATGGTTCTACACA 230
QY 181 GAACTGAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGGTGTGGTGGAGTTCGGCAAGGACGGCGACACCCAC 300
Db 291 GTGGGCTTCAGGACCCCGGGGTGTGGTGGAGTTCGGCAAGGACGGCGACACCCAC 350
QY 301 CTGCTGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
Db 351 CTGCTGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 410
QY 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGGAGTTCGGCAAGGACGGCGACACGAC 420
Db 411 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGGAGTTCGGCAAGGACGGCGACACGAC 470
QY 421 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 480
Db 471 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 530
QY 481 CTGGTGTCTATGTTGCGAGGGGCTCGGCTTCAACCGTGTCCCGCACGGTGGACGG 540
Db 531 CTGGTGTCTATGTTGCGAGGGGCTCGGCTTCAACCGTGTCCCGCACGGTGGACGG 590
QY 541 GGGTTCAACAGCAGCAGCGGGTGAACCTGACCGTGAACGAGGAGCAAGCTGGTGAAG 600
Db 591 GGGTTCAACAGCAGCAGCGGGTGAACCTGACCGTGAACGAGGAGCAAGCTGGTGAAG 650
QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCGCTGTGATCCCC 710
QY 711 GACATGCAAGAGCTTGGCATCAAGGATAGAGACGAGGAGGATCGTTGGCTCGTT 770
Db 771 AAGATCAAACTACTGCGCTGCC 744
152114 152114.1 GI:2473315
LOCUS 152114 1422 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5646026.
ACCESSION 152114
VERSION 152114.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1422)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.B.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5646026-A 16 08-JUL-1997;
FEATURES Location/Qualifiers
source 1..1422
BASE COUNT 420 a 364 c 357 g 281 t
ORIGIN
Query Match 98.8%; Score 740.8; DB 6; Length 1422;
Best Local Similarity 99.7%; Pred. No. 2.9e-103;
Matches 742; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAAGAAATAGTGCACAAAGTTCACCTGAAATCTCCCGTGGAGACGCAACTACCT 60
Db 51 ATGAAAGAAATAGTGCACAAAGTTCACCTGAAATCTCCCGTGGAGACGCAACTACCT 110
```

```
QY 61 TACAGCGCTTCATCGCTGGTCCGGAAGAGAGTATGATCAAACTGCACCGACCATAAA 120
Db 111 TACAGCGCTTCATCGCTGGTCCGGAAGAGAGTATGATCAAACTGCACCGACCATAAA 170
QY 121 GGGATCTTCAGCCCGGTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 180
Db 171 GGGATCTTCAGCCCGGTGCTGCCACCGGAGAGAGTCCCGGAGCTATGGTTCTACACA 230
QY 181 GAACTGAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 240
Db 231 GAGCTCAAACTAGGACCACTCCATCAGCTCGCCATAGCATGGAACCTGTACCTC 290
QY 241 GTGGGCTTCAGGACCCCGGGGTGTGGTGGAGTTCGGCAAGGACGGCGACACCCAC 300
Db 291 GTGGGCTTCAGGACCCCGGGGTGTGGTGGAGTTCGGCAAGGACGGCGACACCCAC 350
QY 301 CTGCTGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 360
Db 351 CTGCTGGCGACAAACCCAGGTGGCTCGGCTTCGGCGGAGGTACAGGACCTCATCGGC 410
QY 361 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGGAGTTCGGCAAGGACGGCGACACGAC 420
Db 411 AACAAAGGTCTGAGACCGTCAACATGGCGCGCGGAGTTCGGCAAGGACGGCGACACGAC 470
QY 421 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 480
Db 471 CTGGCGAAGAGAAAGGCGGTGACCCACAGCGCCGACACAGAGCAAGCAAGCTGGTGAAG 530
QY 481 CTGGTGTCTATGTTGCGAGGGGCTCGGCTTCAACCGTGTCCCGCACGGTGGACGG 540
Db 531 CTGGTGTCTATGTTGCGAGGGGCTCGGCTTCAACCGTGTCCCGCACGGTGGACGG 590
QY 541 GGGTTCAACAGCAGCAGCGGGTGAACCTGACCGTGAACGAGGAGCAAGCTGGTGAAG 600
Db 591 GGGTTCAACAGCAGCAGCGGGTGAACCTGACCGTGAACGAGGAGCAAGCTGGTGAAG 650
QY 601 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCGCTGTGATCCCC 660
Db 651 TGGGACAGGATCTCCAAAGCGGCTTCGAGTGGGCTGACCAACCGCTGTGATCCCC 710
QY 661 GACATGCAAGAGCTTGGCATCAAGGATAGAGACGAGGAGGATCGTTGGCTCGTT 720
Db 711 GACATGCAAGAGCTTGGCATCAAGGATAGAGACGAGGAGGATCGTTGGCTCGTT 770
QY 721 AAGATCAAACTACTGCGCTGCC 744
Db 771 AAGATCAAACTACTGCGCTGCC 794
RESULT 12
144709 144709 1683 bp DNA linear PAT 07-OCT-1997
LOCUS 144709
DEFINITION Sequence 18 from patent US 5635384.
ACCESSION 144709
VERSION 144709.1
KEYWORDS GI:2469422
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1683)
AUTHORS Walsh,T.A., Hey,T.D. and Morgan,A.B.R.
TITLE Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL Patent: US 5635384-A 18 03-JUN-1997;
FEATURES Location/Qualifiers
source 1..1683
BASE COUNT 513 a 419 c 412 g 339 t
ORIGIN
Query Match 98.8%; Score 740.8; DB 6; Length 1683;
Best Local Similarity 99.7%; Pred. No. 2.8e-103;
```


Matches		742;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	ATGAAAGAAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGGAGCGGAACCTACCCCT	60						
Db	51	ATGAAAGAAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGGAGCGGAACCTACCCCT	110						
QY	61	TACAGCGCTTCATCG	CGTTCGCGAAGACGTGATCAAACTGCAACCGACCATAA 120							
Db	111	TACAGCGCTTCATCG	CGTTCGCGAAGACGTGATCAAACTGCAACCGACCATAA 170							
QY	121	GGATCTTCAGCCGCTG	TCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 180							
Db	171	GGATCTTCAGCCGCTG	TCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 230							
QY	181	GAACTGAAACTAGGAC	CAAGCTCCATACGCTCGCCATACGATGACAACTGTACCTC 240							
Db	231	GAGCTCAAACTAGGAC	CAAGCTCCATACGCTCGCCATACGATGACAACTGTACCTC 290							
QY	241	GTGGGCTTCAGACCC	CGCGGGGTGTGGAGTTCGGAAGAACCGGACACCCAC 300							
Db	291	GTGGGCTTCAGACCC	CGCGGGGTGTGGAGTTCGGAAGAACCGGACACCCAC 350							
QY	301	CTCCTCGGCGCAACA	CCCGAGGTGGCTCGGCTTCGGGCGGAGTACAGGACCTCATCGGC 360							
Db	351	CTCCTCGGCGCAACA	CCCGAGGTGGCTCGGCTTCGGGCGGAGTACAGGACCTCATCGGC 410							
QY	361	AACAAGGGTCTGGAG	ACCGTCAACATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 420							
Db	411	AACNAGGGTCTGGAG	ACCGTCAACATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 470							
QY	421	CTGGCGAAGAAGAAC	GGCGGTGACCCACAGGCGGACACGAAAGCAAGCTGTGTGAAG 480							
Db	471	CTGGCGAAGAAGAAC	GGCGGTGACCCACAGGCGGACACGAAAGCAAGCTGTGTGAAG 530							
QY	481	CTGGTGTCTATGTTG	CGAGGGCTGCGGTTCAACCGCTGCCCGACGGTGGACGCG 540							
Db	531	CTGGTGTCTATGTTG	CGAGGGCTGCGGTTCAACCGCTGCCCGACGGTGGACGCG 590							
QY	541	GGGTTCAACAGCAGC	AGCGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 600							
Db	591	GGGTTCAACAGCAGC	AGCGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 650							
QY	601	TGGACAGATCTCAAG	CGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660							
Db	651	TGGACAGATCTCAAG	CGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710							
QY	661	GACATCAGAAGCTTG	GCATCAAGGATAAGACGAGCAGGAGTCTGTGCTCGTT 720							
Db	711	GACATCAGAAGCTTG	GCATCAAGGATAAGACGAGCAGGAGTCTGTGCTCGTT 770							
QY	721	AAGAATCAAACTACT	GCCTGCC 744							
Db	771	AAGAATCAAACTACT	GCCTGCC 794							

RESULT 13
I52115
LOCUS
DEFINITION
Sequence 18 from patent US 5646026.
I52115
VERSION
I52115.1 GI:2473316
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 1683)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
AUTHORS
TITLE
Ribosome-inactivating proteins, inactive precursor forms thereof, a process for making and a method of using
JOURNAL
Patent: US 5646026-A 18 08-JUL-1997;
FEATURES
Location/Qualifiers
1. .1683
/organism="unknown"

BASE COUNT		513 a	419 c	412 g	339 t
ORIGIN					
Query Match		98.8%; Score 740.8; DB 6; Length 1683;			
Best Local Similarity		99.7%; Pred. No. 2.8e-103;			
Matches 742; Conservative		0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGAAAGAAATAGTGC	CAAAAGTTCACTGAAATCTTCCCGTGGAGGAGCGGAACCTACCCCT	60	
Db	51	ATGAAAGAAATAGTGC	CAAAAGTTCACTGAAATCTTCCCGTGGAGGAGCGGAACCTACCCCT	110	
QY	61	TACAGCGCTTCATCG	CGTTCGCGAAGACGTGATCAAACTGCAACCGACCATAA 120		
Db	111	TACAGCGCTTCATCG	CGTTCGCGAAGACGTGATCAAACTGCAACCGACCATAA 170		
QY	121	GGATCTTCAGCCGCTG	TCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 180		
Db	171	GGATCTTCAGCCGCTG	TCCACCGGAGAGAGGTCCCGAGGTATGGTTCTACACA 230		
QY	181	GAACTGAAAACTAGGAC	CAAGCTCCATACGCTCGCCATACGATGACAACTGTACCTC 240		
Db	231	GAGCTCAAACTAGGAC	CAAGCTCCATACGCTCGCCATACGATGACAACTGTACCTC 290		
QY	241	GTGGGCTTCAGAAC	CCCGCGGGGTGTGGAGTTCGGAAGAACCGGACACCCAC 300		
Db	291	GTGGGCTTCAGAAC	CCCGCGGGGTGTGGAGTTCGGAAGAACCGGACACCCAC 350		
QY	301	CTCCTCGGCGCAACA	CCCGAGGTGGCTCGGCTTCGGGCGGAGTACAGGACCTCATCGGC 360		
Db	351	CTCCTCGGCGCAACA	CCCGAGGTGGCTCGGCTTCGGGCGGAGTACAGGACCTCATCGGC 410		
QY	361	AACAAGGGTCTGGAG	ACCGTCAACATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 420		
Db	411	AACAAGGGTCTGGAG	ACCGTCAACATGGCGCGCGGAAATGACAGGGCCGTCAACGAC 470		
QY	421	CTGGCGAAGAAGAAC	GGCGGTGACCCACAGGCGGACACGAAAGCAAGCTGTGTGAAG 480		
Db	471	CTGGCGAAGAAGAAC	GGCGGTGACCCACAGGCGGACACGAAAGCAAGCTGTGTGAAG 530		
QY	481	CTGGTGTCTATGTTG	CGAGGGCTGCGGTTCAACCGCTGCCCGACGGTGGACGCG 540		
Db	531	CTGGTGTCTATGTTG	CGAGGGCTGCGGTTCAACCGCTGCCCGACGGTGGACGCG 590		
QY	541	GGGTTCAACAGCAGC	AGCGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 600		
Db	591	GGGTTCAACAGCAGC	AGCGGGGTGACCTTGACCGTGACGAGGGGAAGCAGGTGCAGAAG 650		
QY	601	TGGACAGATCTCAAG	CGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 660		
Db	651	TGGACAGATCTCAAG	CGCGGCTTCGAGTGGGCTGACACCCACCGCTGTGATCCCC 710		
QY	661	GACATCAGAAGCTTG	GCATCAAGGATAAGACGAGCAGGAGTCTGTGCTCGTT 720		
Db	711	GACATCAGAAGCTTG	GCATCAAGGATAAGACGAGCAGGAGTCTGTGCTCGTT 770		
QY	721	AAGAATCAAACTACT	GCCTGCC 744		
Db	771	AAGAATCAAACTACT	GCCTGCC 794		

RESULT 14
I44711
LOCUS
DEFINITION
Sequence 22 from patent US 5635384.
I44711
ACCESSION
I44711.1 GI:2469424
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 1695)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
AUTHORS
TITLE
Ribosome-inactivating proteins, inactive precursor forms thereof, a

JOURNAL		process for making and a method of using		US 5635384-A 22 03-JUN-1997;	
FEATURES		Location/Qualifiers		1..1695	
source		/organism="unknown"		516 a 422 c 415 g 342 t	
BASE COUNT				516 a 422 c 415 g 342 t	
ORIGIN				1..1695	
Query Match		98.8%; Score 740.8; DB 6; Length 1695;			
Best Local Similarity		99.7%; Pred. No. 2.8e-103;			
Matches 742; Conservative		0; Mismatches 2; Indels 0; Gaps 0;			
QY	1	ATGAAAGAAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT	60	
Db	51	ATGAAAGAAATAGTGC	AAAGTTCACTGAAATCTTCCCGTGGAGGACGCGAACTACCCCT	110	
QY	61	TACAGCGCCTTCATCG	CGTCCGGAAGACGTGATCAAACTGCGACCGACCAATAA	120	
Db	111	TACAGCGCCTTCATCG	CGTCCGGAAGACGTGATCAAACTGCGACCGACCAATAA	170	
QY	121	GGGATCTTCCAGCCGT	GTGCCACCGGAGAAAGTCCCGAGCTATGTTCTACACA	180	
Db	171	GGGATCTTCCAGCCGT	GTGCCACCGGAGAAAGTCCCGAGCTATGTTCTACACA	230	
QY	181	GAACTGAAACTAGGAC	CAAGTCCATACGCTCGCCATACGATGACCAACCTGTACCTC	240	
Db	231	GAGCTCAAAACTAGGAC	CAAGTCCATACGCTCGCCATACGATGACCAACCTGTACCTC	290	
QY	301	CTCCTCGGCGCAACCC	CGGCGGCTTCGCGGCGAGGTACCGAGACCTCATCGGC	360	
Db	351	CTCCTCGGCGCAACCC	CGGCGGCTTCGCGGCGAGGTACCGAGACCTCATCGGC	410	
QY	421	CTGGCGAAGAGAGAGG	CGGTGACCAAGCGCGACACGAGCAAGCTGGTGAAG	480	
Db	471	CTGGCGAAGAGAGAGG	CGGTGACCAAGCGCGACACGAGCAAGCTGGTGAAG	530	
QY	541	GGTTCAACAGCCAGCA	CGCGGTGACCTTGAACCGTGACGGGGAAGCGGTGCGAAG	600	
Db	591	GGTTCAACAGCCAGCA	CGCGGTGACCTTGAACCGTGACGGGGAAGCGGTGCGAAG	650	
QY	601	TGGGACAGGATCTCAA	AGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC	660	
Db	651	TGGGACAGGATCTCAA	AGGCGGCTTCGAGTGGGCTGACCCACCGCTGTGATCCCC	710	
QY	661	GACATGCAGAGCTTGG	CATCAAGGATAGAAACGAGGAGGATCGTTCGGCTCGTT	720	
Db	711	GACATGCAGAGCTTGG	CATCAAGGATAGAAACGAGGAGGATCGTTCGGCTCGTT	770	
QY	721	AAGAATCAAACTACTG	CCGCTGCC 744		
Db	771	AAGAATCAAACTACTG	CCGCTGCC 794		
Search completed: October 22, 2003, 06:15:40					
Job time : 2895 secs					

RESULT 15	152117	LOCUS	1695 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 22 from patent US 5646026.					
ACCESSION	152117					
VERSION	152117.1					GI:2473318
KEYWORDS	Unknown.					
SOURCE						